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RESULT 1
US-07-876-280-30
is Sequence 30, Application US/07876280
is Sequence 30, Application US/07876280
is Patent No. 5262158
is APPLICANT: Cannon, Raymond J.C.
is APPLICANT: Bagley, Angela L.
is TITLE OF INVENTION: Controlling Acarides
is NUMBER OF SEQUENCES: 30
is CORRESPONDENCE ADDRESS:
is ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Plopyy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,280
FILING DATE: 19920430
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REJERAN: 904-375-8100
TELEFAX: 904-375-8100
TYPE: AMINO ACID
STRANDEDNESS: single
TYPE: AMINO ACID
STRANDEDNESS: single
MYDETTER TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:
CLONE: B. coli NM522(pMYC2320) NRRL B-18769
US-07-876-280-30
                        US-07-951-715A-7
US-08-459-5448A-7
US-08-459-504B-7
US-08-459-504B-7
US-09-053-549-8
US-09-547-422-7
US-08-961-803-9
US-07-973-320-2
US-09-641-773-320-2
US-09-641-773-320-2
US-09-641-803-9
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US-07-973-320-4
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US-08-754-490-14
                                                                                                                                                                                                                                                                          ALIGNMENTS
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11186
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ANTI-SENSE: NO
ORIGINAL SOURCE:
2549
2519.5
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2231.389 Million cell updates/sec
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                                                                                                                                                                           1 MSPNNQNEYEILDASSSTSV.......MSETEGVFNIESVELVLEEE 1167
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                                                                                           June 21, 2004, 10:10:21 ; Search time 27 Seconds
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5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-876-280-30

US-07-812-180A-2

US-07-941-650A-2

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US-07-915-203-2

US-08-215-203-2

US-08-215-468-4

US-08-1315-468-4

US-08-1315-468-4

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US-08-1315-468-5

US-08-1315-468-5

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US-08-1315-468-5

US-09-1315-47-5

US-09-002-285-72

US-09-002-285-74

US-09-002-285-74

US-09-002-285-74

US-09-002-285-74

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US-08-880-685-2

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Maximum Match 100%
Listing first 45 summaries
                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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LIBRARY: Lambdagem
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CLONE: 50C
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                                                                                              ETFISSSTVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVED
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                                               1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
                          14;
     Length 1157;
tch 66.3%; Score 4007; DB 1; Length 1 al Similarity 66.1%; Pred. No. 2.3e-285; 773; Conservative 144; Mismatches 238; Indels
 Query Match
Best Local S
Matches 773
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Sequence 2, Application US/07812180A
Patent No. 5366892
GENERAL INFORMATION:
APPLICANT: Foncerrada, Luis R
APPLICANT: Payne, Jewel M
APPLICANT: Payne, Jewel M
APPLICANT: Payne, Jewel M
TITLE OF INVENTION: thuringiensis Isolate and a No. 5366892el Gene Encoding TITLE OF INVENTION: thuringiensis Isolate and a No. 5366892el Gene Encoding NUMBER OF SEQUENTION: Coleopteran-Active Toxin
NUMBER OF SEQUENTION: Coleopteran-Active Toxin
NUMBER OF SEQUENTION: Coleopteran-Active Toxin
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RLOQAWNLYDLRNAI PNGDFRNGLSDWNATSDVNVQQLSDTSVLVI PNWNSQVSQQFTVQ
                                1009 RLOOAWNLYDORNAIPHIELE SNWNATPGVEVQOINHTSVLVIPNWDEQVSQOFTVQ
                                                                                                                                            1069 PNQRYVLRVTARKEGGGGGGYSINDGSGGGGGETLIFSASDYDTNGYNDQTGYITKTVTFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Gaineby---
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BROOM COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS 5.0
COPETWARE: PatentIn Release #1.0, Version #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 66.3%; Score 4007; DB 1; Best Local Similarity 66.1%; Pred. No. 2.3e-285; Matches 773; Conservative 144; Mismatches 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - 11 LIBRARY OF LUIS
                                                                                                                                                                                                                                                     1129 PYTDQMWIEISETEGTFYIESVELIVDVE 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Roman Saliwanchik
STREET: 2421 N.W. 41st Street, Ste A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/812,180A
FILING DATE: 19220102
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, Roman
TELECHOWNICATION INFORMATION:
TELEPHOWE: 904-375-8100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICA: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
CREANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PSSOC
IMMEDIATE SOURCE:
IMMEDIATE SOURCE:
CREANISM: Ramamotoensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PSSOC
IMMEDIATE SOURCE:
1019
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/08/315,468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:
LIBRRAY: Lambdagem (TM) - 11 LIBRARY OF LUIS
CLONE: 50C(a)
1129 PYTDQMWIEISETEGTPYIESVELIVDVE 1157
                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION UNBER: 1953
FILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/808,316
FILING DATE: 16-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA73.C2
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                  Sequence 2, Application US/08315468
Patent No. 5554534
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELRFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
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STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                         AKIPSFAISGOEVPLLSVYAQAANLHLLLRDASIFGAEWGFTPGEISTFYDRQVTRTAQ 240.
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    241 YSDYCVKWYKIGLDKLKGTTSKSWLNYHQPRREWTLLVLDLVALPPNYDTHMYPIETTAQ
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1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP 1 MSPNNONEYEIIDATPSTSVSSDSNRYPFANBPTDALQNWNYKDYLKWSGGENPELFGNP 14; Query Match

66.3%; Score 4007; DB 1; Length 1157;
Best Local Similarity 66.1%; Pred. No. 2.38-285;
Matches 773; Conservative 144; Mismatches 238; Indels 14 APPLICANT: Michaels, Tracy Ellis
APPLICANT: Michaels, Luis
APPLICANT: Michaels, Luis
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Process for Controlling Scarab Pests
TITLE OF INVENTION: with Bacillus thuringiensis Isolates
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA FONCERRADA

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1129 PYTDOMWIEISETEGTFYIESVELIVDVE 1157
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                               Sequence 2, Application US/07941650A
Patent No. 6294184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                       US-07-941-650A-2
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AKIPSFAISGQEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQVTRTAQ
                                                                                                          SIPSFAVSGHEVLLLAVYAQAVNLHLLLLRDASIFGEEWGFTPGEISRPYNRQVOLTAE
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                                                          YSDYCVKWYNTGLDKLKGTNAASWLKYHOPRREMTLLVLDLVALFPNYDTRTYPIETTAQ
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                                         LIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFV
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APPLICANT: Uyeda, Kendrick A.
APPLICANT: Bradfisch, Gregory A.
TITLE OF INVENTION: Process for Controlling Lepidopteran Pests
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,650A
FILING DATE: 19920908
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/941,650A
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/758,020
FILING APPLICATION NUMBER: US 07/758,020
FILING DATE: 12-SEP-1991
PRIOR APPLICATION NUMBER: US 07/658,935
FILING DATE: 21-FEB-1991
PRIOR APPLICATION NUMBER: US 07/642,112
FILING DATE: 16-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: SA11,wanchik, David R.
REGISTRATION NUMBER: US 17,94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 66.3%; Score 4007; DB 3; Best Local, Similarity 66.1%; Pred. No. 2.3e-285; Matches 773; Conservative 144; Mismatches 238;
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STREET: 2421 N.W. 418t Street, Suite i
CITY: Gainesville
STATE: FL
COUNTRY: USA
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STRAIN: kumamotoensis
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                                                                          YSDYCVKWYNTGLDKLKGTNAASWLKYHOFRREMTLLVLDLVALFPNYDTRTYPIETTAO
                                                                                                                                                         LPLINNTEYLEYWVGHSIKYKNT-NASSALERNYGTITSNKIKYYDLANKDIFQVRSLGAD
                                                                                                                                                                                                                                          LSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVYSDKITQIPVVKAH
                                                                                                                                                                                                                                                                                                536 MLYLGGSVVQGPGFTGGDILKRTNPSILGTPAVTVNGSLSQRYRVRIRYASTTDPB-FTL
                                                                                                                                                                                                                                                                                                                             ISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGEVYVD
                                                                                                                                                                                                                                                                                                                                                                                                              NEKRMLWDAVKEAKRLVQARNLLQDTGFNRINGENGWTGSTGIEVAEGDVLFKDRSLRLT
                                 AKIPSFAISGQEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQVTRTAQ
                                                                                                                  LTREVYTDPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSEIEFYTTRAG
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RESULT 5

21; 181 RTHMGSFSQTHYETPLLPTYAQAASLHLLVMRDVQIYGKEWGYPQNDIDLFYKEQVSYTA 240 299 241 RYSDHCVQWYNAGLNKLRGTGAKQWVDYNRFRREMNVWVLDLVALFPNYDARIYPLETNA 300 QLIREVYIDPIVFNRETSGGFCRRWSLN----SDI-----SFSEVESAVIRSPHLFDIL 349 :||||::|||: ELTREIFTDPV-----GSYVTGQSSTLISWYDMIPAALPSFSTLEN-LLRKPDFFTLL 352 9 9 61 ETFISS-STVOTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVE DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDF **OYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLLVLDLVALFPNYDTRTYPIETTA** 1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP 180 VAKIPSFAISGOEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQVTRTA APPLICANT: Kawasugi, Tadaaki TITLE OF INVENTION: No. 5359048el Microorganism and Insecticide NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: DB 1; Length 1149; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OOPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/915,203
FILING DATE: 19920723
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REGISTRATION INFORMATION:
TELEBHONE: 904-375-8100
TELEBHONE: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS: Query Match 60.6%; Score 3662.5; DB 1; Best Local Similarity 63.8%; Pred. No. 4.6e-260; Matches 752; Conservative 109; Mismatches 257; ADDRESSEE: David R. Saliwanchik STREET: 2421 N.W. 41st Street, Suite CITY: Gainesville STATE: F. COUNTRY: US APPLICANT: Obba, Michio
APPLICANT: Iwahana, Hidenori
APPLICANT: Sato, Reiichi
APPLICANT: Sato, Reiichi
APPLICANT: Gyiwara, Katsutoshi
APPLICANT: Gakanaka, Kazunobu
APPLICANT: Gakanaka, Kazunobu
APPLICANT: Asano, Shouji 2, Application US/07915203). 5359048 1149 amino acids MOLECULE TYPE: protein AMINO ACID linear 32606 TOPOLOGY: ; MOLECULE T US-07-915-203-2 120 240 300 301 ઠ g

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INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 1149 amino acids
TYPE: amino acid
                                                                          STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d.
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MOLECULE TYPE: protein
NUMBER OF SEQUENCES:
                                                               Gainesville
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Best Local Simil
Matches 752; (
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               SEIEFYTTRAGLPLNNT-EYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKYYDLANK 408
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                                                                                                 627 GISGSSRTFDISITKEAGAANLYIDRIEFIPVNTLFEAEBLDVAKKAVNGLFTNEKDAL
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                                             353 QEIRMYTS---FRONGTIEYYNYWGGQRLTLSYIYGSSP--NKYSGVLAGAEDIIPVGQN
                                                                              DIFOVRSLGADLANYYAQVYGVPYASFTLLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNT
                                                                                                                                           469 ID---EIPPENEPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVY
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APPLICANT: Ogiwara, Katsutoshi
APPLICANT: Sakanaka, Kazunobu
APPLICANT: Hori, Hidetaki
APPLICANT: Asano, Shouji
APPLICANT: Kawasugi, Tadaaki
TITLE OF INVENTION: No. 5747450el Microorganism and Insecticide
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Patent No. 5747450
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Iwahana, Hidenori
Sato, Relichi
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APPLICANT: INAMANA,
APPLICANT: Sato, Re
APPLICANT: Suzuki,
APPLICANT: Ogiwara,
APPLICANT: Ogiwara,
APPLICANT: History
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indela
                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.6%; Score 3662.5; DB 1;
ilarity 63.8%; Pred. No. 4.6e-260;
Conservative 109; Mismatches 257;
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
                                                                                                                                                                                                                                    CURRIT ARE: CERCILLII ALICERE #1.0, VER CURRIT ARE: CERCILLII ALICERE WAS APPLICATION NUMBER: US/08/22,887
FILING DATE: 08-UUL-1994
CLASSIFFCATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/915,203
FILING DATE: 23-UUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAILWANCHIK, DAVIG
REGISTRATION NUMBER: 31.794
REFERENCE/DOCKET NUMBER: 31.794
TELECHMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
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21;

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GenCore version 5.1.6
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                     Copyright
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OM protein - protein search, using sw model

June Run on:

21, 2004, 10:10:20 ; Search time 30 Seconds (without alignments) 3741.850 Million cell updates/sec

US-10-089-678-1 Title: Perfect score: Sequence:

1 MSPNNQNEYEILDASSSTSV.....MSETEGVFNIESVELVLEEE 1167 Scoring table:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
1: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES			
Result No.	Score	Query Match	Length	DB	ID	Description	ď	
-	3733.5	61.8	1160	7	I40589	parasporal	crystal	
7	3123	51.7	1157	Н	S49247	parasporal	crystal	
٣	2750.5	45.5	1154	7	539536	parasporal	crystal	
4	2547.5	42.1	1228	N	S00873	parasporal	crystal	
2	2458.5	40.7	1138	N	A48944	parasporal	crystal	
9	2191	36.3	1156	7	S19306	parasporal	crystal	
7	2154.5	٠ س	1174	7	A42459	parasporal	crystal	
æ	2093.5	34.6		~	S32645	parasporal	crystal	
σ	2064.5	34.2		~	A26513	parasporal	crystal	
10	2061.5	34.1		~	JD0002	parasporal	crystal	
11	2052.5	٠		~	S02134	parasporal	crystal	
12	2048	•		7	JT0241	parasporal	crystal	
13	2045	33.8		~	JC2219	parasporal	crystal	
14	2044.5	33.8	1181	7	A41052	parasporal	crystal	
15	2043	•		~	A29125	parasporal	crystal	
16	2038	ω.		7	802215	parasporal	crystal	
17	2037	33.7	1176	7	A22617	parasporal	crystal	
18	2030.5	33.6		~	139838	parasporal	crystal	
19	2024.5	33.5		~	140572	parasporal	crystal	
20	2010.5	33.3	٦	~	A37829	parasporal	crystal	
21	1989.5	32.9	7	~	S32649	parasporal	crystal	
22	1984	32.8		N	S00944	parasporal	crystal	
23	1953.5	32.3	1160	~	S32647	parasporal	crystal	
24	1944	32.2	_	7	S11446	parasporal	crystal	
25	1939	ď	~		USBSXH	parasporal	crystal	
26	1932	'n	-	~	A29838	parasporal	crystal	
27	1930.5	31.9		N	A49785	parasporal	crystal	
28	1923.5	31.8	-	7	A48970	parasporal	crystal	
29	1917	31.7	1172	~	S32689	parasporal	crystal	

parasporal crystal parasporal crystal parasporal crystal	cryV465 protein - insecticidal prote parasporal crystal insecticidal prote	parasporal crystal parasporal crystal parasporal crystal parasporal crystal	
USBSBI 139870 A26858	140590 139815 S25383 139814	A22798 S04181 I39811 S10228	B29838 JH0261 JC7140 B42459
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30.9 29.4 29.3	28.7 28.5 28.4 28.3	27.9 23.4 21.1 20.8	18.7 17.7 17.6
1868.5 1778.5 1772.5	1734.5 1722.5 1713.5 1707.5	1683.5 1413 1272.5 1258.5	1132.5 1116.5 1069.5 1061
30 31 32	3.3 3.5 3.5 3.5	C 8 6 6 4 4	. 4 4 4 4 1 5 6 4 5

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140589
parasporal crystal protein cry8Cal - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryll1
C;Species: Bacillus thuringiensis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 01-Dec-2000
C;Accession: 140589
R;Sato, R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; Asan
Curr. Microbiol. 28, 15-19, 1994
A, Title: Cloning, heterologous expression, and localization of a novel crystal protein

A;Trie: Cioning, mererologous expression, and localization of a movel cry A;Reference number: 140589; MUID:94100786; PMID:7764305 A;Accession: 140589 A;Actures : preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1160 «RES-A;Cross-references: EMBL.U04366; NID:9532523; PIDN:AAA21119.1; PID:9532524 C;Superfamily: parasporal crystal protein C;Keywords: delta-endotoxin

21; 240 299 349 61 BTPISS-STVOTGIGIVGOVLGALGVPPAGQIASPYSPIVGQLWPSSTVSVWEMIMKQVB 119 120 DLIDOKITDSVRKTALAGIQGIGDGLDVYOKSLKNWLENRNDTRARSVVVTQYIALELDF 179 180 VAXIPSFAISGQEVPLLSVYAQAANIHLILLRDASIFGAEWGPTPGBISTFYDRQVTRTA 239 241 RYSDHCVQWYNAGLNKIRGTGAKOWVDYNRFRREMNVMVLDLVALFPNYDARIYPLETINA 300 301 ELTREIFTDPV-----GSYVTGQSGTLISMYDMIPAALPSFSTLEN-LLEKPDFFTLL 352 350 SBIBFYTTRAGLPLANT-EYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKYYDLANK 408 353 QEIRMYTS---FRQNGTIEYTNYWGGQRLTLSYIYGSSF--NKYSGVLAGAEDIIPVGQN 407 9 9 181 RINMGSFSQTNYETPLLETYAQAASLHLLVWRDVQIYGKEWGYPQNDIDLFYKBQVSYTA 300 QLTREVYTOPIVENRETSGGFCRRWSLN----SDI-----SFSEVESAVIRSPHLFDIL 240 QYSDYCVKWYNTGLDXLKGTNAASWLXYHQFRREMTLLVLDLVALFPNYDTRTYPIETTA 1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP Gaps Query Match 61.8%; Score 3733.5; DB 2; Length 1160; Best Local Similarity 64.2%; Pred. No. 1.6e-208; Matches 767; Conservative 109; Mismatches 257; Indels 61; 셤 g ઠ g ð 셤 ò 셤 ð g 셤 Š ઠે 8

409 DIPQVRSLGADLANYYAQVYGVPYASFTLLDKWTGSGSVGGFTYSKPHTTMQVCTQNYNT 468

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paragporal crystal protein cryBal - Bacillus thuringiensis subsp. thuringiensis N;Alternate names: parasporal crystal protein cryA4 (;Species: Bacillus thuringiensis subsp. thuringiensis (;Species: Bacillus thuringiensis subsp. thuringiensis (;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Dec-2000 (;Accession: S00873 **Ribrizard, B.L.; Whiteley, H.K.**
Nicleic Acids Res. 16, 2721-2724, 1988 A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus A;Reference number: S00873; MUID:88203216; PMID:3362680
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                                           RNLLQDTGFNRING--ENGWTGSTGIEVAEGDVLFKDRSLRLTSAREIDTETYPTYLYQQ
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                     DLTFNTFDLATIGTAFTFSNYSDSLTVGADSPASGGEVYVDKPELI PVNATFEAEEDLDV
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A;Cross-references: EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g580949
C;Genetics:
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Pred. No. 1.3e-139;
3; Mismatches 381; Indels 151;
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43.8%;
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C;Superfamily: parasporal cr
C;Keywords: delta-endotoxin
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A; Molecule type: DNA
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N;Alternate names: delta-endotoxin-related protein; parasporal crystal protein cryX
N;Alternate names: delta-endotoxin-related protein; parasporal crystal protein cryX
S;Species: Bacillus thuringiensis
C;Date: 07-06c1-1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
C;Accession: S39536
R;Shevelev, A.B.; Svarinsky, M.A.; Karasin, A.I.; Kogan, Y.N.; Chestukhina, G.G.; Stepan
FEBS Lett. 336, 79-82, 1993
A;Fitle: Primary structure of the cryX, the novel delta-endotoxin-related gene from Baci
A;Reference number: S39536
A;Accession: S39536
A;Accession: S39536
A;Accession: S39536
A;Accession: S39536
A;Residues: DNA
A;Residues: 1-1154 <SHB:
C;Steparfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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                                             PNWNSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDDDTGVLS 1124
                                                                     SHWDAQVSQQLRVNPNCKYVLRVTARKVGGGDGYVTIRDGAHHQETLTFNACDYDVNGTY 1114
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IPGINYEIYTELSDRLQQASYLYTSRNAVQNGDFNSGLDSWNTTMDASVQQDGNMHFLVL 1054
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දු දු	121 LIDOKITDSYRKTALAGLOGLODYQKSIKOWIERRNDTRARSYVTQYIALBLDPY 180	q
8	AKIPSPAISGQEVPLLSVYAQAANLHLLLLRDASIPGAEWGFTPGBISTFYDRQVTRTAQ	충 용
g G	NAMPLFAIRNQEVPLLMVYAQAANLHLILLLRDASLFGSBFGLTSQBIQRYYERQVBRTRD	
සි ර	241 YSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREWTLLVLDLVALPPNYDTRTYPIBTTAQ 300 [RES A48 par
ò	301 LTREVYTDPIVPNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSEIBFYTTRAG 360	α. α. α. α.
qa	282 LTREVITDAIGATGVRMASMNWYNNNAPSFSAIEAAAIRSPHILDFLEQLTIFSAS 337	S C S
ò	LPLANTEYLEYMVGHSIKXKNTNASSALBRNYGTITSNKIKYYDLANKDIFQVR	App A;T
DP DP	338 SRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRFASRDVYRTE 391	A,R
<u>ک</u> ک	415 SIGADLANYYAQVYGVPASFTLLDKATGSGSVGGFTYSKPHTTMQVCTQNYNTIDEI 472 302 SVAGUTIAGTYTRDIHAYDVTDBNFTNDANYGND-GTANYGNDVEGDTAINGRFT-R1, 448	4 ;44 α;α
3 8	DDE NEDI CECTORIE CONTROL CHITECON CONTROL	4
· 점		A CO
ò	531 QIPVVKAHTLVSGTTVIKGPGPTGGNILKRISSGPLAYTSVSVKSPLSQRYRARIRYAST 590	χ, (
qa	501 QIPMVKASELPQGTTVVRGPGPTGGDILERTNTGGFGPIRVTVNGPLTQRYRIGFRYAST 560	2 A C
ò	591 INLALEVIISGTRIYSINVNKTWAKGDDLIPNIPDLATIGTAFTFSNYSDSLIVGADSPA 650	£ &
qa	561 VDFDFFVSRGGTTVNNFRFLRTMASDELKYGNFVRRAFTTPFTFTQ1QD11RTS1QGLS 620	3 6
<i>6</i> 8	SGGEVYVDKFELIPVNATFEAREDLDVAKKAVNGLFTSKKD-ALGTSVTDYQVNQAANLV	ò
G ,	GNGEVIIDAIEIIPVIAIFEABIDLEKAQEAVNALFININPKKLKIDVIUXHIDŲVSNLV	g G
රි සි	710 BCLSDELYPHERRALMADAVKBARALQARNILODIGFNRIN	ò
}	-CENCENCE TENDESTINI PRODUCTO IN CARPT DIFFUSIONI VIOLENTI VIOLENDATI	ф
5 음	OSEHGWAGSENITIQEGNDVPKENYVTLPGTFNECYPTYLYQKIGESEKAYTRYOL QSEHGWAGSENITIQEGNDVPKENYVTLPGTFNECYPTYLYQKIGESEKAYTRYOL	È
Š		අු
qq		ð 1
Š	866 ALENNGENG-NMSSDSHAFSFHIDTGEIDLABINGIWVVFKIPTINGYATLGALELVEG 924	8 &
셤	856 DLDCSCRDGEKCAHHSHHFSLDIDVGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEK 915	g
<i>8</i> ∶	925 PLSGETLERAQQQEQQWQDKWARKRGASEKAYYAAKQAIDRLFADYQDQKLMSGVEMSDM 984	ò
QQ Q		q
λ i	985 LAAQNLVQSIPYVYNDALPEIPGKNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSD 1044	δ
<u> </u>	HAADKLVHKIKKAIISKLFVIFGVNAKIFKKLKHIITAISLIDAKNVVKNGDFNNGLIC	g
& &	WNATSDVNVQQLSDTSVLVIPNWNSQVSQQPTVQPNYRYULRYTARKEGVGDGYVIIRDG	Š
g 8	WOVEGHUOUQQSHRKSDLV1FEWEABVSQAVKVCFGCGILLKVIAIREGIGEGCVIINE.	đ
è i	ANQUELUTE	È
QQ	1096 ENNIDELKKKNKEEEESVIKIDIGICNDITAHGGIAGCADACASKNAGIEDAIEVUITASV 1155	

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Accession: A48944
Liambert, B.; Hofte, H.; Annye, K.; Jansens, S.; Soetaert, P.; Peferoen, M.
Liambert, B.; Hofte, H.; Annye, K.; Jansens, S.; Soetaert, P.; Peferoen, M.
ppl. Environ. Microbiol. 58, 2336-2542, 1992
Ifitle: Novel Bacillus thuringiensis insecticidal crystal protein with a silent activi
Reference number: A48944; MUID:92384571; PMID:1514800
Contents: BTS137J
Accession: A48944
61 BTFISSSTVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVED 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 LIREVYTDPVSLSIS------NPDIGPSFSQMENTAIRTPHLVDYLDBLYIXTSK 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rasporal crystal protein cry7Aal - Bacillus thuringiensis
Alecrate names: parasporal crystal protein cryIIIC
Species: Bacillus thuringiensis
Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSPNNQNBYBILDASSSTSVSDNSVRYPLANDQTTTLQNWNYKDYLRMSEGENPELPGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: GB-M64478; NID:g142760; FIDN:AAA22351.1; PID:g142761
Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBIP:112093)
Superfamily: parasporal crystal protein
Keywords: delta-endotoxin
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40.7%; Score 2458.5; DB 2; Length 3
Best Local Similarity 43.5%; Pred. No. 1.6e-134;
Matches 514; Conservative 208; Mismatches 400; Indels
                                                                                                                                                            | ::||||:| ||
1216 FIVDSVELLIMEE 1229
                                                                                                                         1155 FNIRSVELVLEER 1167
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Molecule type: DNA; protein
Residues: 1-1138 <LAM>
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A;Note: sequence extracted from NCBI backbone (NCBIN:92865, NCBIP:92867) C;Genetics: A;Gene: crylG C;Superfamily: parasporal crystal protein C;Keywords: delta-endotoxin	Query Match 36.3%; Score 2191; DB 2; Length 1156; Best Local Similarity 41.5%; Pred. No. 5.7e-119; Matches 501; Conservative 195; Mismatches 414; Indels 98; Gaps 24;	QY S NONEYEILDASSTSVSDNSVRYPLANDQTTTLQNMUYKDYLRMSEGENPELFGNPETFI 64	Qy 65 SSSTVQTGIGIVGQVLGALGVP-FAGQIASFYSFIVGQLMPSSTVSVWB 112	QY 113 MIMKQVEDLIDQKITDSVRKTALAGLGGGGGDGLDVYQKSLKNWLENRNDTRARSVVVTQY 172 : : : :	QY 173 IA-LELDFVAKIPSFAISGQSVPLLSVYAQAANLHLALRDASIFGAEWGF 222	QY 223 TPGEISTFYDRQVTRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLLVLD 280	Qy 281 LVALPPNYDTRTYPIETTAQL/TREVYTDPIVFNRETSGGFCRRWSLNSD1SF 332	QY 333 SEVESAVIRSPHLFDILSBIBFYTTRAGLPLN-NTEYLEYWGHSIKYKNTNASSALBRN 391 : : : :	Qy 392 YGTITSNKIKYYDLANKDIPQYRSLGADLANYYAQVYGVPYASFTLLDKNTGSG 445	446 SVGGFT 443 YIRTTG 504 RYGNLP 495 RRSSLV 64 GPLAYT 623 TFPLAY 613 SFAIRE 683 NGLFTS 673 ASLFTR 743 DTGFNR 743 DTGFNR 743 DTGFNR 744 DTGFNR 801 LKFYTR
Db 502 AVRAYKLDDPSTVVKGPGFTGGDLVKRGSTGYIGDIKATVNSPLSQKYRVRVRYRTNVSG 561 Qy 594 KLFVTISGTRIYSINVNKTMAKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADS 648 : : : : : : : : :	Qy 649 FASGGEVYVDKPELIPVNATFEAEBDLDVAKKAVNGLFTSKKDALÇTSVTDYQVNQAANL 708 ::	Qy 709 VECLSDELYPHEKRALMDAVKEAKRLVQARNILQDYGFNRINGENGWTGSTGIEVAEG 766	Qy 767 DVLFKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFIGSSQDLEIKLIRH 926 :	QY 827 RANQIVKNVPDNILLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNRSDSHAFSFH 886 197 PARGILSDSDNILLPDILPENTCGEPNRCAAQQYLDENPSPRCSSMQDGILSDSHSFSLN 856	Qy 887 IDTGEIDLARATGIWUVFKIPTINGYATLGALELVEEGPLSGETLERAQQQEQQWQDKMA 946	CY 947 RKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIFYVYNDALPBIF 1006 : :	Qy 1007 GWNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIPN 1066- 	OY 1067 WNSQVSQOFTVQPNYRYULRVTARKEGVGDGYVIIRDGANQTETLTPNICDDDTGVLSAD 1126	Qy 1127 QTSYITKTVEFTBSTBQVWIDMSBTBGVFNIESVELVLEBE 1167 :	SULT 6 9306 Alterna Species Species Species Saulevi

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1111 SYTDGRRDNPCESNRGYGDYTPLPAGYVTKELBYFPETDKVWIEIGETEGTFIVDSVELL 1170
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              SGTIDSLDEIPPQDNSGAPWNDYSHVLMHVTFVRWPGEISGSDSW-RAPMFSWTHRSATP 455
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C;Species: Bacillus thuringiensis
C;Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C;Accession: S32645
R;Lambert, B.
submitted to the EMBL Data Library, April 1993
A;Reference number: S32645
A;Accession: S32645
                                                                                                                                                  G-NMSSDSHAPSPHIDTGRIDLNENTGIWWVPKIPTTNGYATLGNLBLVBBGPLSGBTLE
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TONYNTIDEIPPENEPLS--RGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADV
                                                 TNTVYSDKITQIPVVKAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSQR
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A;Residues: 1-1166 <LLMN-
A;Cross-references: BMBL:Z22510; NID:g295861; PIDN:CAA80233.1; PID:g295862
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71
                                                            1029 NGLDSWNATAGASVQQDGNTHPLVLSHWDAQVSQQFRVQPNCKYVLRVTAEKVGGDGTV
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                                                                                                               NGLSDWNATSDVNVQQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYV
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                                                                                                                                                                                                                   1160 VELVLEEE 1167
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Query Match 34.6%; Score 2093.5; DB 2; Length 1166; Best Local Similarity 39.7%; Pred. No. 2.7e-113; Matches 482; Conservative 172; Mismatches 392; Indels 167; Gaps 24;	59 NPETFISSSTVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLMPSSTVSVW 111	112 EMIMKQVEDLIDQKITDSVRKTALAGLGGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQ 171 2. :: :	YIALELDFVAKI PSPAISGOEVPLLSVYAQAANLHLLLLRDASI FGAENGFRSGERVATR YIALELDFVAKI PSPAISGOEVPLLSVYAQAANLHLLLLRDASI FGAENGFTFGEISTFY	DRQVIRTAQYSCVKNYNTGLDKLKGTNAASNLKYHOFRRENTLAUDLVALEPNYDTR :	TYPIBITAQLTREVYTDDIVFNRETSGGFCRRWSLNSDISFSEVBSAVIRSPHLPDILSE	352 IEFYTTRAGLPLANTEYLEYWVGHSIKYKNTNASSALERNYGT 394	395 ITSNKIKYYDLANKDIPQVRSLGADLANYYAQVYGVPYASFTLLDKNTGSGSVGGFT-YS 453	454 KPHTTMQVCTQNYNTIDEIPPENBFLSRGYSHRLSHITSYSFSKNASSPARYGNLPVF 511	512 AWTHRSADVINTVYSDKITQIPVVKAHTLVSGTTVIKGPGFTGGNILKRISSGPLAYTSV 571 :	572 SVKSPLSGRYRARIRYASTTNLRLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGT 631 :::	632 AFTPSNYSDSLTVGADSFASGGEVYVDKFELIPVNATPRAREDLDVAKKAVNGLFTSKKD 691 : : :	692 -ALÇTSVTDYQVNQAANLVECLSDBLYPNEKRMLWDAVKBAKRLVQARNLLQDTGFNRIN 750	751GENGWTGSTGIEVAEGDVLFKDRSLRLTSAREIDTETYPTYLYQQIDBSLLKPYTRYK 808	809 LKGFIGSSQDLEIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDAN 864	865 LALENNGENG-NMSSDSHAFSFHIDTGEIDLMENTGIWVVFKIPTTNGYATLGNLELVEE 923	924 GPLSGETLERAQQQGQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ	KPLLGBALARVKRABKKWRDKRBKLELETNIVYKBAKBSVDALFVNSQYDQLQADTNIAM	984 MILAQNIVOSIPYVRNDALPEIRGMNYTSFTELTNRLQQAWNIYDLRNAIPNGDFRNGLS 1043 :
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poral crystal protein - Bacillus thuringiensis (strain aizawai)
ccies: Bacillus thuringiensis
cs: 11-Mar-1988 #sequence_revision 11-Mar-1988 #text_change 01-Dec-2000
session: A26513
h, K.; Oshie, K.; Shimizu, M.; Nakawura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H. 53, 113-119, 1987
cle: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis ierence number: A26513; MUID:87248103; PMID:3297927
98 IVGQLWPSSTVSVWEMIMKQVBDLIDQKITDSVRKTALAGLQGLQGLGVYQKSLKAWLE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 IWGIFGPSQ----WDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAGSFREWEA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 NRNDTRARSVVVTQYIALELDFVAKIPSFAISGOEVPLLSVYAQAANLHLLLLRDASIFG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 AEMGFTPGEISTFYDRQVTRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338 AV---IRSPHLPDILSEIBFYTTRAGLPLNNTEYLEYWVGHSIK-----YKWTNASSALE 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 RNYGTITSNKIKYYDLANKDIFQVRSLGADLANYYAQVY--GVPYASFTLLDKNT----G 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 444 SGSVGGFTYSKPHTTMQVCTQNYNTIDBIPPENB--PLSRGYSHRLSHITSY--SFSKNA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500 SSPARYGNLPVPAWTHRSADVTNTVYSDKITQIPVVKAHTLVSGTTVIKGPGFTGGNILK 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ry Match 34.2%; Score 2064.5; DB 2; Length 1155; t Local Similarity 39.0%; Pred. No. 1.3e-111; ches 476; Conservative 184; Mismatches 387; Indels 173; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              idues: 1-1155 <0BD>
ss-references: GB:N16463; NID:g143098; PIDN:AAA22551.1; PID:g143099
erfamily: parasporal crystal protein
words: delta-endotoxin
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1154 FIVESVELLAMBE 1166
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scule type: DNA
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A;Status: preliminary
A;Molecule type: DNA
A;Cross-teferences: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
A;Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
B;Hofte, H.; de Greve, H.; Senrinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerc
Bur. J. Biochem. 161, 273-280, 1986
A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thu
A;Reference number: A26461; MUID:87054026; PMID:3023091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 AEWGFTPGEISTFYDRQVTRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLL 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residuse: 1-730,'L',732-784,'R',786-1155 <HOP>
A;Cross-references: GB:X04698; NID:g40254; PIDN:CAA28405.1; PID:g40255
A;Experimental source: strain berliner 1:15
C;Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 IWGIFGPSQ----WDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRNDTRARSVVVTQYIALELDPVAKIPSPAISGOEVPLLSVYAQAANLHLLLLRDASIPG
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                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-1155 < WAB>
A; Residues: 1-1155 < WAB>
A; Cross-references: GB:M13898; NID:g142719; PIDN:AAA22330.1; PID:g142720
A; Cross-references: GB:M13899. berliner
B; Chak, K.F.; Jen, J.C.
R; Chak, K.F.; Jen, J.C.
A; Description: Complete nucleotide sequence and expression in Escherichia A; Reference number: S14555
A;Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:g143124
A;Experimental source: subsp. kurstaki
R;Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.
                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 34.1%; Score 2061.5; DB 2; Length 1155; Best Local Similarity 39.3%; Pred. No. 1.9e-111; Matches 478; Conservative 185; Mismatches 387; Indels 167;
                                                                                                                                     sequence
                                                                                      DNA 5, 305-314, 1986
A;Title: Bacillus thuringiensis entomocidal protoxin gene A;Reference number: A90955; MUID:86300092; PMID:3743328
A;Accession: A90955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: cry.1-2; bt2
C; Superfamily: parasporal crystal protein
C; Keywords: delta-endotoxin
F; 82-586/Product: toxic peptide #status predicted <TXP>
F; 82-300/Region: toxic #status predicted
F; 82-300/Region: insecticidal #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S14555
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C;Genetics:
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parasporal crystal protein crylAb3 - Bacillus thuringiensis
NyAlternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal processions Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 01-Dec-2000
C;Accession: A90025; A91565; S14555; A26461; A24172; A29043; JD0002
R;Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.
Agric. Biol. Chem. 51, 455-463, 1987
A;Title: Cloning and mucleotide sequencing of two insecticidal delta-endotoxin genes from A;Reference number: A90025
A;Accession: A90025
A;Accession: A90025
A;Accession: A90025
A;Residues: 1-1155 cKON>
A;Experimental source: subsp. kurstaki
B;Geiser, M.; Schweizzer, S.; Grimm, C.
Gene 48, 109-118, 1986
A;Title: The hypervariable region in the genes coding for entomopathogenic crystal prote
A;Reference number: A91560; MUD:87163505; PMID:3557124
A;Accession: A91560
A;Molecule type: DNA
A;Residues: 1-1155 cGEI>
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                 Single
                                                                                                                                                                34.0%; Score 2052.5; DB 2; Length 1155; 39.4%; Pred. No. 6.3e-111;
                                                                                                             and
J. Mol. Biol. 208, 183-194, 1989
A; Title: Functional mapping of an entomocidal delta-endotoxin. A; Ritle: Functional mapping of an entomocidal delta-endotoxin. A; Recession: 804994; MUID:89362455; PMID:2769751
A; Rocession: 804994
A; Rolecule type: DNA
A; Residues: 429-449; A*, 451-724 «HAW>
A; Cross-references: BrMBL:X16315
A; Experimental source: strain alzawai IC1
C; Comment: This toxin is lethal to the larvae of lepidopterans C; Reywords: delta-endotoxin
C; Keywords: delta-endotoxin
                                                                                                                                                                                            Indels
                                                                                                                                                                              al Similarity 39.4%; Pred. No. 6.3e-111; 479; Conservative 183; Mismatches 388;
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N;Alternate names: delta-endotoxin ICl; entomocidal crystal protein
C;Species: Bacillus thuringiensis
A;Variety: strain aizawai ICl
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C;Accession: S02134; S04994
R;Haider, M.Z.; Ellar, D.J.
Nucleic Acids Res. 16, 10927, 1988
A;Title: Nucleotide sequence of a Bacillus thuringiensis aizawai ICl entomocidal cry
A;Accession: S02134
A;Accession: S02134
A;Accession: S02134
A;Accession: S02134
A;Cross-reference: EMB::X13233; NID:940277; PIDN:CAA31620.1; PID:940278
A;Experimental source: Expair aizawai ICl
R;Haider, M.Z.; Ellar, D.J.
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                                                                                            PGQISTLRVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSG
                                                                                                                                         920 LVEEGPISGETIERAQQQEQQWQDKWARKRGASEKAYYAAKQAIDRLFADYQDQKINSGV
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                               NGLPTSKKD-ALQTSVTDYQVNQAANLVBCLSDELYPNBKRMLWDAVKBAKRLVQARNILL
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                                                                                                                                                                                                                                                    158 NRNDTRARSVVVTQYIALELDFVAKIPSFAISGQEVPLISVYAQAANLHLLLLRDASIFG 217
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A;Accession: JC2219
A;Molecule type: DNA
A;Residues: 1-1176 <UDA>
A;Residues: 1-1176 <UDA>
A;Cross-references: DDBJ:D17518; NID:g506190; PIDN:BAA04468.1; PID:g535781
C;Genetics:
A;Gene: crytA(a)
A;Gene: crytA(a)
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
                                                                                                                                                         53 NPEL-----PGNPET-FISSSTVQTG---IGI---VGQVLGALGVPPAGQIASFYSF
                                                                                                                                                                      NYGTITSNKIKYYDLANKDIPQVRS-----LGADLANYYAQVYGVPYASPTLLDKNT
                                                                                                         Query Match 33.8%; Score 2045; DB 2; Length 1176; Best Local Similarity 39.3%; Pred. No. 1.8e-110; Matches 479; Conservative 174; Mismatches 415; Indels 152;
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parasporal crystal protein cryAel - Bacillus thuringiensis (strain alesti)
C;Species: Bacillus thuringiensis
B;Lee, C.S.; Aronson, A.I.
J. Bacteriol. 173, 6615-6618, 1991
A;Title: Cloning and analysis of delta-endotoxin genes from Bacillus thuringiensis subs
A;Title: Cloning and analysis of delta-endotoxin genes from Bacillus thuringiensis subs
A;Title: Cloning and analysis of delta-endotoxin
A;Recession: A41052
A;Atatus: Preliminary
A;Status: Preliminary
A;Residues: 1-1181 <LEBS
A;Cross-references GB:M65252; NID:g142874; PIDN:AAA22410.1; PID:g142875
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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                                  857 ARLGNLEFLEEKPLVGBALARVKRAEKKWRDKREKLEWETNIVYKBAKESVDALFVNSQY
                                                                                                                                1119 DTGVLSADQTS-----YITKTVEFTPSTEQVWID
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ATLGNLELVEEGPLSGETLERAQQDEQUMODXWARKRGASEKAYYAAKQAIDRLFADYQD
                                                                                                      OKLINSGVEMSDMLAAQNLVQSIPYVYNDALPEIPGMYTSFTELTNRLQQAWNLYDLRNA
                                                                                                                                                                                                                                                                                                                                                        EGYGEGCVT I HEI ENNYTDELKPSNCVEEE I YPNNTVTCNDYTVNQEEYGGAYTSRNRGYN
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979 VEMSDMLAAQNLVQSIPYVYNDALPEIPGANYTSFTELTNRLQQAWNLYDLRNAIPNGDF 1038
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                                                                Length 1156;
                                                              Query Match
33.8%; Score 2043; DB 2;
Best Local Similarity 39.1%; Pred. No. 2.2e-110;
Matches 476; Conservative 185; Mismatches 389;
C;Superfamily: parasporal crystal protein C;Keywords: delta-endotoxin
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C;Species: Bacillus thuringiensis subsp. kurstaki
C;Species: Bacillus thuringiensis subsp. kurstaki
C;Species: Bacillus thuringiensis subsp. kurstaki
C;Accession: A29125
R;Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Bio/Technology S; 807-mail, 1987
A;Title: Insect tolerant transgenic tomato plants.
A;Reference number: A29125
A;Accession: A29125
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-1156 <PIS>
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  GTMGNAAPQQRIVAQLGQGVYRTLS---STFYRNPFIIGINNQRLSVLDGTBFAYGSSSN 395
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                                               VGGFTYSKPHTTMQVCTQNYNTIDBIPPE--NEPLSRGYSHRLSHITSY--SPSKNASSP
                                                                                                                                     ARYCHL PVPAWTHRSADVTNTVYSDKITQI PVVKAHTLVSGTTVI KGPGFTGGNI LKRTS
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Search completed: June 21, 2004, 10:13:10 Job time : 37 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

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1	CRAA BACUK STANDARD; PRT; 1157 AA.
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DŢ	2001 (Rel.
H	(Re].
占	(Rel. 40, Last annotation update)
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DE	protein).
Š	CRYBAA OR CRYVIIIA(A).
ဗ	Bacillus thuringiensis (subsp. Kumamotoensis).
ဗ	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
ŏ	NCBI_TaxID=132267;
N.	[1]
RP	
2	STRAIN=NRRL B-18746 / PS50C;
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RT	gene encoding a coleopteran-active toxin.";
Z	Patent number BP0498537, 12-AUG-1992.
ដ	-i- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
ប្រ	EPITHELIAL CELLS OF COLEOPTERA.
5	DEVELOPMENTAL STAGE: The crystal protein is produced during
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3 5	-1- MISCRIANNOIS. Toxic segment of the protein is located in the N-
3 5	termina
3 6	Letwinson Belond to the delta endotoxin family
3 5	
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ບ	or send an email to license@isb-sib.ch).
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ä	EMBL; U04364; AAA21117.1;
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3	porulation.
S	SEQUENCE 1157 AA; 131009 MW; 687B5C49DE93683B CRC64;
8	66.38;
Ä	sal Similarity 66.1%; Pred. No. 1.1e-220;
Ma	Matches 773; Conservative 144; Mismatches 238; Indels 14; Gaps

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                                                                                                                                                                                                                     LPLNNTEYLEYWVGHSIKYKNT-NASSALERNYGTITSNKIKYYDLANKDIFQVRSLGAD 419
                                                                                                                                                                                                                                                                   LSRGYSHRLSHITSYSFSKNASSPARYGNLPVPAWTHRSADVTNTVYSDKITQIPVVKAH 538
                                                                                                                                                                                                                                                                                                                                                             SERVERSHRITSHITSHSFSKXKS-AYYGSFPVFVWTHTSADLNNTIYSDKITQIPAVKGD 535
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                                                                                                                                                                                                                                                                                                                                                                                                           536 MLYLGGSVVQGPGFTGGDILKRINPSILGTFAVTVNGSLSQRYRVRIRYASTTDFE-FTL 594
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                                                                   LIDOKITDSVRKTALAGLOGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFV 180
                                                                                                                                                             YSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLLVLDLVALFPNYDTRTYPIBTTAQ 300
                                                                                                                                                                                                                                                                                                    LANYYAQVYGVPYASPTLLDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTIDBIPPENB-P 478
MSPNNQNBYEIIDATPSTSVSSDSNRYPFANEPTDALQNMNYKDYLKMSGGENPELFGNP 60
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE OF 1-14 AND 56-64, AND CHARACTERIZATION.

SEQUENCE OF 1-14 AND 56-64, AND CHARACTERIZATION.

MINEMALINE-94259659; PubMed-8200856; PubMed-8200856; PubMed-8200856; PubMed-8200856; PubMed-8200868.

MINEMALMAL ABANO S., Sato R., Ohba M., Iwahana H., Suzuki N., Anano S., Sato R., Ohba M., Iwahana H., Suzuki N., Anano S., Sato Barveidal toxin protein from Bacillus Thuringienais servor japonensis strain Buibui specific for scrabaeid beetles.";

J. Appl. Bacteriol. 76:307-313(1994).

J. Appl. Bacteriol. 76:307-313(1994).

J. Appl. Bacteriol. 76:307-313(1994).

PUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT STRAIN AND MARIAN CUPREA, A. RUPOCUPREA AND POPILLIA JAPONICA.

SUCH AS ANOMALA CUPREA, A. RUPOCUPREA AND POPILLIA JAPONICA.

C. I. DEWELDPHENTAL STAGE: The crystal protein is produced during sportlation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sato R., Takeuchi K., Ogiwara K., Minami M., Kaji Y., Suzuki N., Hori H., Asano S., Ohba M., Iwahana H.;
"Cloning, heterologous expression, and localization of a novel crystal protein gene from Bacillus thuringiensis serovar japonensis strain buibul toxic to scarabaeld insects.";
Curr. Microbiol. 28:15-19(1994).
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MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry8Ca (Insecticidal delta-endotoxin CryVIIC(a)) (Crystaline entomocidal protoxin) (130 kDa crystal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis (subsp. japonensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
NCBI_TaxID=128936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   terminus.
SIMILARITY: Belongs to the delta endotoxin family.
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llarity 64.2%; Pred. No. 4.4e-205;
Conservative 109; Mismatches 257;
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PSTEQVWIDMSETEGVFNIBSVELVLEER
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InterPro; IPR008979; Gal_bind_like.
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MEDLINE=94100786; PubMed=7764305;
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InterPro; IPR005638; endotoxin_C.
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HSSP; P07130; IDLC.
                                                                                                                                                                                                                                         STANDARD;
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SEQUENCE 1160 AA;
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SEQUENCE FROM N.A.
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InterPro: IPR005638; endotoxin.C.
InterPro: IPR005639; endotoxin.N.
InterPro: IPR008979; Gal_bind_like.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: PROMOTES COLLOIDOSWOTIC INSIS BY BINDING TO THE MIDGUT
-!- ENTITELIAL CELLS OF INSECTS. ACTIVE ON VARIOUS SCARABARID BEBTLES.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSPNNQNBYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Michaels T.E., Foncerrada L., Narva K.E.; "Process for controlling scarab pests with Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pesticidial crystal protein crysBa (Insecticidal delta-endotoxin
cryvIIIB(a)) (Crystaline entomocidal protoxin) (134 kDa crystal
                                                                                       84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1169;
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52.2%; Score 3152; DB 1; Length 1
Best Local Similarity 54.0%; Pred. No. 6.4e-172;
Matches 653; Conservative 179; Mismatches 294; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00555; endotoxin; 1.
Pfam; PF03944; endotoxin C; 1.
Pfam; PF03945; endotoxin N; 1.
Toxin; Sportlation.
SEQUENCE 1169 AA; 133543 MW; 22EEPCF5BD699909 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus
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Bacteria; Firmicutes; Bacillales; Bacillaceae;
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                           QLIREVYTDPIVPNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSBIBFYTTRA 359
                                                                                                                                                                                                                                               360 GLPLANTEYLEYWCHSIKYKNTNASSALERNYGT-----ITSNKIKYYDLANKDIPQVR 414
                                                                                                                                                                                                                                                                                   S--PTSDRYMRYWAGHQISYKHIGTSSTFTQMYGTNQNLQSTSN----PDFTNYDIYKTL 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                934 AQQQEQOMQDKWARKKGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQS 993
BLINQKIAEYARNKALSELEGLGNNYQLYLTALEEWKENPNGSRALRDVRNRFEILDSLF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQLSDTSVLVI PNWNSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVI IRDGANQTETLTP
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                                                                                                                         | | | | : : | | | : : : : | | SNGAVLLDIVYPGYTYTFFGMPETEFFWVNQLMNTRKT--LTY-KP-ASKDIDRTREDSB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSSODLEIKLIRHRANGIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALENNGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1114 NICDDDTGVLSADQTS----YIT-----KTVEPTPSTEGVWIDMSETEGVFNI
                                   180 VAKIPSFAISGQEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQVTRTA
                                                     QYSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLLVLDLVALPPNYDTRTYP1ETTA
                                                                                                                                                                                                                                                                                                                    SLGADIAN ----YYAQVYGVPYASPTILIDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTI
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

STRAIN=BTSO2618A;
NEDLINE=S0141404; PubMed=8572715;
NEDLINES DESCRIPTION PROMOFRS COLORIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT EPUTENIAL CELLS OF LEPIDOFTERA LARVAR. HAS A FAIRLY BROAD SPECTRUM OF ACTIVITY AGAINST MEMBERS OF THE PAMILIES PYRALIDAE, PUTENIALDAE, SPRINGIDAE, AND NOCTUIDAE IT IS THE PIRST INSECTICIDAL CRYSTAL PROTEIN WITH ACTIVITY AGAINST CUTWORMS. NO ACTIVITY IS OBSERVED AGAINST SOME BEEFLES, SUCH AS COLORADO POTATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the spore cost. MISCRILANDOUS: Toxic segment of the protein is located in the
                                                                                  CryixC(a)) (Crystaline entomocidal protoxin) (130 kDa crystal protein).

protein).

Crysta (A).
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SEQUENCE 1157 AA; 129775 MW; C364391EF7FDFBBA CRC64;
                                                                                                                                                            Bacillus thuringiensis (subsp. tolworthi).
Bacteria; Pirmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 52.3%; Pred. No. 2.8e-170;
Matches 619; Conservative 195; Mismatches 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.7%; Score 3123; DB 1; 52.3%; Pred. No. 2.8e-170;
                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-CT-2010 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry9Ca (Insectici
1157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, P07130; IDLC.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PP00555; endotoxin.1.
Pfam; PP03944; endotoxin.C; 1.
Pfam; PF03945; endotoxin.C; 1.
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PIR; A59350; S49247.
HSSP; P07130; 1DLC.
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 C9CA BACTO
045733;
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SHWDAQVSQQLRVNPNCKYVLRVTARKVGGGGGYVTIRDGAHQSTLTFNACDYDVNGTY 1114
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                                                                    592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLPLNNTEYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKY---YDLANKDIPQVRSL 416
                                                                                                                                                                 - PPV-SSNPMDYWSGHTLRRSYLNDSAVQEDSYGLITTTRATINPGVDGTNR----IEST 413
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                                                                                                                                                                                                             | : :||| ||| || || AVDFRSALIGIYGVNRASFVPGGLFNGTTSPANGG------CRDLYDTNDBLPP 461
                                                                                                                                                                                                                                                                                                                                                                                                      NLVECLSDBLYPNEKRMLMDAVKEAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVA 764
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LRLFVTISGTRIYSINVNKTMNKGDDLTFNTF---DLATIG---TAPTFSNYSDSLTVGA
                                                                                                                                                                                                                                                                                                                                                                       RHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMSSDSHAFS
                                                                                                                                                                                                GADLANYYAQVYGVPYASPTL - - LDXNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP
                                                                                                                                                                                                                                                                               PVVKAHTLVSGTTVIKGPGFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTN
                              VAKI PSPAISGQEVPLLSVYAQAANLHLLLLRDASI PGAEWGPTPGBISTPYDRQVTRTA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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                                                                                                                                                                                                                                                       Midoh N., Oyama K.;
"Bacillus thuringiensis cry gene for insecticidal crystal protein.";
Submitted (PEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT BPITHELIAL CELLS OF INSECTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                          the spore coat. MISCELLANBOUS: Toxic segment of the protein is located in the
                                           16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry9Ea (Insecticidal delta-endotoxin CryIXE(a)) (Crystaline entomocidal protoxin) (130 kDa cry8tal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 1150;
                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: The crystal protein is produced dui sporulation and is accumulated both as an inclusion and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                          Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the delta endotoxin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.7%; Score 2825.5; DB 1;
llarity 48.6%; Pred. No. 2.6e-153;
Conservative 197; Mismatches 364;
                                                                                                                                                        Bacillus thuringiensis (subsp. aizawai).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
NCBI_TaxID=1433;
               1150
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InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal bind like.
PF00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB011496; BAA34908.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PP03944; endotoxin_C; 1. Pfam; PP03945; endotoxin_N; 1.
               STANDARD;
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                                                                                                                                              CRY9EA OR CRYIXE(A)
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Matches 574; Conserv
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SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLIDOKITDSVRKTALAGLOGIGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDF 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 TQFMPSFG-SGPGSQNYATILLPVYAQAANLHLLLKDADIYGARWGLNQTQIDQFHSRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSBIEP---YTTRAGLPLANYTEYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKYYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANKDI PQVRSLGADLANYYAQVYGVPYASFTLLDKNTGSGSVGGPTYSKPHTTMQVCTQN
                                                             nitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT BPITHELLIAL CELLS OF INSECTION.
BEVELCOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                 the spore coat. MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1169;
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SEOURNCE 1169 AA; 132228 MW; 659AB257229DE5E9 CRC64;
                                                                                                                                                           terminus.
SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.9%; Score 2715; DB 1; larity 46.9%; Pred. No. 5.3e-147; Conservative 204; Mismatches 383;
                                                                                                                                                                                                                                                                                                                                InterPro; IPR001178; Endotoxin.
InterPro; IPR005629; endotoxin.C.
InterPro; IPR005629; endotoxin N.
InterPro; IPR008979; Gal_bind_like.
                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PP00555; endotoxin; 1.
Pfam; PF03944; endotoxin C; 1.
Pfam; PF03945; endotoxin N; 1.
                                                                                                                                                                                                                                                                                                      D85560; BAA19948.1; -.
                                                    Asano S.;
Submitted (MAY-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                     P07130: 1DLC
 NCBI_TaxID=128936;
                          SEQUENCE FROM
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RLTISRNRYTAPTTNS-PLDYWSGHTLQSQHANNPTTYBTSYGQITSN-TRLFNTTN-GA
                                                                                          FOVRSLGADLANYYAQVYGVPYASPTLLDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTID
                                                                                                          TISPVVNLPVNNSAA---GPTLPSTWAQNGSLTYESPNTLEVTHTIRFSQSDTTLRLNIP
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry9Da (Insecticidal delta-endotoxin CryIXD(a)) (Crystaline entomocidal protoxin) (132 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOTSYITKTVEFTPSTEQVWIDMSETBGVFNIESVBLVLEER 1167
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CRY9DA OR CRYIXD(A).
Bacillus thuringiensis (subsp. japonensis).
Bacteria; Pirmicutes; Bacillales; Bacillaceae; Bacillus.
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                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 40, Last annotation update)
16-OCT-2010 (Rel. 40, Last annotation update)
Pesticidial crystal protein crylka (Insecticidal delta-endotoxin
CrylKa)) (Crystaline entomocidal protoxin) (137 kDa crystal protein)
CRYLKA OR CRYLK(A) OR CRYLK.
Bacillus thuringlensis (Subsp. morrisoni).
Bacillus pirmicutes; Bacillales; Bacillaceae; Bacillus.
                                 YRARIRYASTINLALPVTISGTRIYSINVNKTMNKGDDLTPNTFDLATIGTAFTFSNYSD
                                                                                                                SLTVGADSPASGGEVYVDKFELIPVNATFEAEEDLDVAKKAV-NGLFTSKKDALQTSVTD
                                                                                                                                                                                                          STGIEVAEGDVLFKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFIGSSQ
RNSTDELPSLNPEGD-IIRNYSHRLSHITQYRPQATQSGSPSTVSANLPTCVWTHRDVDL
                        TNTVYSDKITQI PVVKAHTLVSGTTVI KGPGPTGGNI LKRTSSGPLAYTSVSVKSPLSQR
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MEDLINE=56,102856; PubMed=8586263;
MEDLINE=56,102856; PubMed=8586263;
Koo B.T., Park S.-H., Choi S.-K., Shin B.S., Kim J.I., Yu J.H.;
Koo B.T., Park S.-H., Choi S.-K., Shin B.S., Kim J.I., Yu J.H.;
Koo B.T., Park S.-H., Choi S.-K., Shin B.S., Kim J.I., Yu J.H.;
Forbing of a novel crystal protein gene cry1K from Bacillus
thuringiensis subsp. morrison!";
FERS Microbiol. Left. 134:159-164(1995).
-!- FUNCTION: PROMOTES COLLADOGNATIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF INSECTS. SELECTIVELY TOXIC TO ARTOGEIA RAPAE
AND NOT ACTIVE ON PLOTELLA XYLOSTELLA.
-!- DEVELOPMENTAL STARE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part o
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outeration the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MISCELLANEOUS: Toxic segment of the protein is located
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                                    SIMILARITY: Belongs to the delta endotoxin family
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ilarity 46.3%; Pred. No. 6.4e-147;
Conservative 194; Mismatches 351;
                                                                                                                                                                                                                                                                    InterPro; IPR001178; Endotoxin.
InterPro; IPR005639; endotoxin C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal bind like.
Pfam; PF00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 1215 AA; 137378 MW;
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Matches 581; Conserv
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InterPro; IRR001178; Endotoxin.
InterPro; IRR005639; endotoxin_C.
InterPro; IRR005639; endotoxin_N.
InterPro; IRR008979; Gal_bind_like.
Pfam; PP00555; endotoxin; 1.
Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endotoxin_N; 1.
                                                                                                                                                                         1229 AA; 139769 MW;
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                                                      EMBL; L32020; AAA22344.1;
HSSP; P02965; 1CIY.
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             SDELYPNEKRMLWDAVKEAKRLVQARNILLQDTGFNRING--ENGWTGSTGIEVAEGDVLF
                                                          SDEFCLDKKRELLEBVKYAKRLSDERNLLQDPTFTSISGQTDRGWIGSTGISIQGGDDIF
                                                                                                                                         IVKNVPDNLLP----DVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMS-SDSHAFSF
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein crylBb (Insecticidal delta-endotoxin
CrylB(b)) (Crystaline entomocidal protoxin) (140 kDa crystal protein)
CRYLBB OR CRYETS.
Bacillus thuringlensis.
Bacteria: Firmicutes; Bacillales; Bacillus.
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STRAIN=NRRL B-21110 / EG5847;

DOMOVAN W.B., Tan Y., Jany C.S., Gonzalez J.M. Jr.;

DOMOVAN W.B.

Bacillus thuringlensis cryet4 and cryet5 toxin genes and proteins toxic to lepidopteran insects.";

Patent number US5322687, 21-JUN-1994.

-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT ENTELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.

-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sportlation and is accumulated both as an inclusion and as part
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MISCELLANEOUS: Toxic segment of the
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                                                                                                                                                                                                                                                                                                                                                                                           Indels 140;
                                                                                                                                                                                                                                                                                                                                                Length 1229;
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                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 43.2%; Pred. No. 1.1e-137;
Matches 548; Conservative 205; Mismatches 375;
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NATSDVNVQQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGA 1105
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-ENGWTGSTGIEVAEGDVLFKDRSLRLTSARBIDTETYPTYLYQQIDBSLLKPYTRYKLK 810
                                                                                                                                                                                                                                      LSGETLERAQQQEQQWQDKMARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDML 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF INSECTS.
DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                      GFIGSSQDLEIKLIRHRANQIVKNVP--DNLLPDVL--PVNSCGGIDRCSEQQYVDANLA
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                                                                                           SEHGWWGSANVTIQEGNDVFKENYVTLPGT---PNECYPNYLYQKIGESELKAYTRYQLR
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kDa crystal protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis (subsp. kurstaki), and Bacillus thuringiensis (subsp. entomocidus).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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01-NOV-1986 (Rel. 09, Created)
01-NAY-2000 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein crylba (Insecticidal of CrylB(a)) (Crystaline entomocidal protoxin) (140 | CRYIBA OR CRYIB(A) OR CRYAA.
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Soetaert P.;
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                                                                                                                                                                                                                                                                                                                    42.1%; Score 2547.5; DB 1; Length 1228; 43.8%; Pred. No. 2e-137;
                                                                                                                                                                                                                                                                                                                                               Matches 558; Conservative 183; Mismatches 381; Indels 151;
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                                                                                                       EMBL; X06711; CAA29898.1; -.
EMBL; X95704; CAA65003.1; -.
ELR; S00873; S00873.
HSSP; P07130; 1DLC.
INTERPRO; IPR001178; Endotoxin.
INTERPRO; IPR005638; endotoxin.C.
INTERPRO; IPR006979; Gal bind like.
Pfam; PP00555; endotoxin.1.
Pfam; PP00345; endotoxin.1.
Pfam; PP00345; endotoxin.7; 1.
Pfam; PP00345; endotoxin.7; 1.
Pfam; PP00345; endotoxin.N; 1.
Toxin; Sporulation.
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the spore coat. MISCELLANBOUS: Toxic segment of the protein is located in the

SIMILARITY: Belongs to the delta endotoxin family

terminus.

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Z46442; CAAB6568.1;
P02965; ICIY.
                                                                                                                                        Toxin; Sporulation
SEQUENCE 1233 AA
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PLLGEALSRVKRAEKKWADKREKLQLETKRVYTEAKRAVDALFVDSQYDRLQADTNIGMI
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                              PLSGETLERAQQQEQQWQDKMARKRGASBKAYYAAKQAIDRLFADYQDQKLNSGVEMSDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein crylBc (Insecticidal delta-endotoxin
CrylB(c)) (Crystaline encomocidal protoxin) (140 kDa crystal protein)
CRY1BC OR CRYIB(c) OR CRYIBC.
                                                           -GENGWTGSTGIEVAEGDVLPKDRSLRLTSARBIDTETYPTYLYQQIDESLLKPYTRYKL
                                                                                                                                         ALENNGENG-NMSSDSHAPSFHIDTGBIDLNENTGIWVVPKIPTTNGYATLGNLELVBEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Bishop A.H., Bone E.J., Ellar D.J.;
"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
Submitted (NVV-1994) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
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DEVELOPMENTAL STAGE: The crystal protein is produced dur sporulation and is accumulated both as an inclusion and
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Bacceria; Pirmicutes; Bacillales; Bacillaceae; Bacillus.
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                   ECLSDBLYPNBKRMLWDAVKRAKRLVQARNLLQDTGFNRIN-
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1216 PIVDSVELLLMER 1228
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@abb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ery Match 41.2%; Score 2491; DB 1; St Local Similarity 42.1%; Pred. No. 3.4e-134; tches 536; Conservative 208; Mismatches 384;
                                                                                                                                                                                Incerpro; IPR001178; Endotoxin.
Interpro; IPR005639; endotoxin_C.
Interpro; IPR005639; endotoxin_N.
Interpro; IPR008979; Gal_bind_like.
Fram; PP00555; endotoxin_1.
Fram; PP03944; endotoxin_C; 1.
Fram; PP03945; endotoxin_N; 1.
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InterPro; IPR001178;
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                                                                                                                                                                                                                 NATSDVNVQQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGA 1105
                                                                                                                                                     985
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                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=NRRL B-18872 / PS158C2;
STRAIN=NRRL B-18872 D.A., Cannon R.J.C., Narva K.E., Stelman S.;
Payne J.M., Cummings D.A., Cannon R.J.C., Narva K.E., Stelman S.;
Bacillus thuringiensis genes encoding lepidopteran-active toxins.";
Patent number US5723758, 03-MAR-1996
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
-BETTHELIAL CELLS OF MANY LEPIDOPTERAN LARVAB.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sportlation and is accumulated both as an inclusion and as part of the spore coat.
-!- MISCELLANBOUS: Toxic segment of the protein is located in the N-

    ENGWIGSTGIEVAEGDVLPKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLK

              GPIGSSODLEIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSBQQ----YVDANLA
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                                                                                                                                                                                                     986 AAQNLVQSIPYVYNDALPEIPGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein crylBe (Insecticidal delta-endotoxin
CrylB(e)) (Crystaline encomocidal protoxin) (139 kDa crystal protein)
CRY1BE OR CRYIB(B) OR 158C2B.
                                                                                                   LENNGENG-NMSSDSHAFSFHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVEEGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               terminus.
SIMILARITY: Belongs to the delta endotoxin family.
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1222 IVDSVELLIMBE 1233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pMYC2383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKIPSFAISGQEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGBISTFYDRQVTRTAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 -RWSNTQYMNYWVGHRIESRTIRGSLSTSTHGNTNTSINPVTLQPTSRDVYRTESPAGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 NYESYSHRISNIRLIS------GNTLRAPVYSWTHRSADRINTISSDSITQIPLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVT1SGTR1YSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGBV
                                                                                                                                                                                                                                                                                                        1 MSPNNONEYEILDASSSTSVSDNSVRYPLANDOTTTLONMNYKDYLRMSEGENPELFGNP
                                                                                                                                                                                                                                                                                                                                LIDOKITDSVRKTALAGLOGLGDGLDVYQKSLKNWLBNRNDTRARSVVVTQYIALBLDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 LPLANTEYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKYYDLANKDIFQVRSLGADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 ANYYAQVYGVPYASFILLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPPE--NEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479 LSRGYSHRLSHITSYSFSKNASSPARYGN---LPVPAWTHRSADVTNTVYSDKITQIPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            536 KAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSGRYRARIRYASTTNLRL
                                                                                                                                                                                                                                                                    Indels 134;
                                                                                                                                                                                                                                Length 1227;
                                                                                                                                                                                          CBA847BEA0B34CD3 CRC64;
                                                                                                                                                                                                                            40.7%; Score 2462; DB 1; Local Similarity 42.9%; Pred. No. 1.5e-132; es 542; Conservative 196; Mismatches 392;
                                                                                                                                                                                                                                                                                                                                                                                                        =
                                                      InterPro; IPR005638; endotoxin C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal bind like.
Pfam; PP00555; endotoxin 1.
Pfam; PP03944; endotoxin C; 1.
Pfam; PP03945; endotoxin N; 1.
Toxin; Sporulation; Plasmid.
                                                                                                                                                                                            139084 MW;
AF077326; AAC32850.1;
P07130; 1DLC.
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Query Match
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                                                                                                                                                                    LVQSIPYVYNDALPEIPGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATS 1049
                                                                                                                                                                                                                             1050 DVNVQQLSDISVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTE 1109
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                                                                       CRDGEKCAHHFSHHFSLDIDVGCIDLHENLGVWVVFKIKTQEGHARLGNLRFIEEKPLLGE
                                                                                                                            924 ALSRVKRARKKWRDKREKLQLETKRVYTEAKRAVDALFVDSQYDRLQADTNIGMIHAADK
                                                                                                                                                                                    MEDLINE=92384571; PubMed=1514800; Lambert B., Fofte H., Annys K., Jansens S., Soetaert P., Peferoen M., Lambert B., Hofte H., Annys K., Jansens S., Soetaert P., Peferoen M., Wovel Bacillus thuringiensis insecticidal crystal protein with a silent activity against coleopteran larvae."; Appl. Environ. Microbiol. 58:2536-2542(1992).
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT PUNCTION: PROMOTIC TO CLEOPTERA. THIS PROTEIN IS NOT TOXIC IN ITS NATURAL PORM. IT IS HIGHLY TOXIC TO COLORADO POTATO BESTLE LARVAE APTER AN IN VITRO SOLUBILIZATION AND TRYPSIN ACTIVATION STEP.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
SSQDLEIKLIRHRANQIVKNVP - - DNLLPDVL - - PVNSCGGIDRCSEQQYVDANLALENN
              806 DSQDLEIYLIRYNAKHETLDVPGTBSVWPLSVESPIGRCGEPNRCA--PHFEWNPDLDCS
                                                                                                             930 TLERAQQQEQQWQDKMARKRGASEKAYYAAKQAIDRLPADYQDQKLNSGVEMSDMLAAQN
                                                                                                                                                                                                                                                                                   ----ADQTS-----
                                                                                                                                                                                                                                                                                                              1104 ELKFKNCEEBEVYPTDTGTCNDYTAHQGTAACNSRNAGYEDAYEVDTTASVNYKPTYEEE
                                                                                                                                                                                                                                                                                                                                          ------YITKTVEFTPSTEQVWIDMSETEGVFNIESVELV
                                                      GENG-NMSSDSHAPSFHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVEEGPLSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the spore coat. MISCELLANBOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Besticidial crystal protein cry7Aa (Insecticidal delta-endotoxin CryVIIA(a)) (Crystaline entomocidal protoxin) (129 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1138 AA
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CRY7AA OR CRYVIIA(A) OR CRYIIIC.
                                                                                                                                                                                                                                                                                   1110 TLTFNICDD-----DTGVLS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTREVYTOPIVENRETSGGFCRRWSLNSDI--SFSEVESAVIRSPHLFDILSEIEFYTTR 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 YKAPSHBIQPDLFYWSAHKVSFKKSBQSNLYTTGIYGKTSGYISSGAYSFHGNDIYRTLA 398
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                                                                                                                                                                                                                                                                                                                                                                   61 ETPISSSTVQTGIGIVGQVLGALGVPFAGQIASPYSFIVGQLWPSSTVSVWEMIMKQVBD
                                                                                                                                                                                                                                                                                                                                                                                                                                             476 NEPLSRGYSHRLSHITSYSPSKNASSPARYGN--LPVFAWTHRSADVTNTVYSDKITQIP
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                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                   Length 1138;
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                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                   40.7%; Score 2458.5; DB 1;
llarity 43.5%; Pred. No. 2.2e-132;
Conservative 208; Mismatches 400;
                                                               InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; endotoxin.N.
Pfam; PP00555; endotoxin,1.
Pfam; PP03944; endotoxin,C; 1.
Pfam; PP03945; endotoxin,N; 1.
Toxin; Sporulation.
EMBL; M64478; AAA22351.1; -.
EMBL; A07236; CAA00646.1; -.
PIR; A48944; A48944.
HSSP; P07130; LDLC.
InterPro; IPR001178; Endotox
                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                           514;
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SEQUENCE
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Toxin; Sporulation.
SEQUENCE 1138 AA;
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                                                                                                                                            GMNYTSPTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIPN 1066
                                                                                                                                                                                       WNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDDDTGVLSAD 1126
                                                                                                                                                                                                 RKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPEIP 1006
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                                                                                                                                                      IDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVEEGPLSGETLERAQQQEQQWQDKMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Payne J.M., Fu J.M.;
"Coleopteran-active Bacillus thuringiensis isolates and genes encodin coleopteran-active toxins.";
Patent number USE2586486, 15-FEB-1994.
-I- FUNCTION: PROXOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF COLLOIDOSMOTIC PROFERS.
-I- DEVELOPMENTAL STAGE: The crystal protein is produced during aporulation and is accumulated both as an inclusion and as part (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the spore coat.
MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry7Ab (Insecticidal delta-endotoxin CryVIIA(b)) (Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus thuringiensis (subsp. dakota).
Bacteria; Pirmicutes; Bacillales; Bacillus
                                                                                                                                                                                                                                 1127 QTSYITKTVEFTPSTEQVWIDMSETEGVPNIESVELVLEEE 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                            1096 ISGYITKELBFPPDTEKVHIBIGETEGIFLVESIBLFLAMEE
                                                                                                                                                                                                                                                                                                            PRT; 1138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR00178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR008639; endotoxin_N.
InterPro; IPR008979; Gal_bind_Tike.
Pfam; PP00555; endotoxin_1.
Pfam; PP03944; endotoxin_C, 1.
Pfam; PP03945; endotoxin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U04367; AAA21120.1; -. HSSP; P07130; 1DLC.
                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                        protein).
CRY7AB OR CRYVIIA(B)
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=132268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YKAPSHBIQPDLFYWCVHKVSFKKSBQSNLYTTGIYGKTSGYISSGAYSFRGNDIYRTLA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             416 LGADLANYYAQVYGVPYASFTLLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDEIPPE 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               533
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                                                                                                                                                                                                                                    121 LIDOKITDSVRKTALAGLOGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALBLDFV 180
                                                                                                                                                                                                                                                                                                                      YSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLLVLDLVALPPNYDTRTYPIBITAQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIREVYIDPIVENREISGGFCRRWSLNSDI--SFSEVESAVIRSPHLFDILSEIEFYTIR 358
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                                                                                                                                                                                                                                                                                                                                                                                                          SYMPSFRVAGYEIPLLTVYAQAANLHLALLRDSTLYGDKWGFTQNNIBENYNRQKKHISE
                                                                                                                            1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTTQNMNYKDYLRMSEGENPELFGNP
                                                                                                                                                  ----SVSG--LFNVFINDBIALQKNFQSTVETIGEGKDLTYGSFGYIBYSTTIQFPNEHP
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                                                                                 Gape
                                                                                 75;
                                          Length 1138;
                                                                                 Indels
01DF7072C074CB88
                                     / Match 40.7%; Score 2458.5; DB 1; Local Similarity 43.1%; Pred. No. 2.2e-132; Les 512; Conservative 218; Mismatches 384;
129778 MW;
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                                      1059 TSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKBGVGDGYVIIRDGANQTBTLTFNICDD 1118
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                        NDALPEI PGMNYTSPTELTNRLQQAMNLYDLRNA I PNGDFRNGLSDWNATSDVNVQQLSD
                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein crylBd (Insecticidal delta-endotoxin
CrylB(d)) (Crystaline encomocidal protoxin) (140 kDa crystal protein).
CRY1BD OR CRYIB(D) OR CRYLAI OR CRYEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSPNNQNBYEILDASSSTSVSDNSVRYPLANDQTTTTLQNMNYKDYLRMSEGENPELPGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLITY, Microbiol, 40:227-222(2000).
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE. TOXIC TO PLUTELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: Toxic segment of the protein is located in the
                                                                                                                                                                                                                                                                                                                                                                                                                       Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.; "Cloning of two new cry genes from Bacillus thuringiensis subsp
                                                                                                                               1119 DIGVLSADQTSYITKTVEFTPSTEQVWIDMSETEGVFNIESVELVLEER 1167
                                                                                                                                               DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 40.5%; Score 2445; DB 1; Length 1231; Best Local Similarity 42.0%; Pred. No. 1.4e-131; Matches 537; Conservative 205; Mismatches 377; Indels 160;
                                                                                                                                                                                                                                                                                                                             Bacillus thuringiensis (subsp. wuhanensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=52024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the delta endotoxin family.
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InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal_bind_like.
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20153386; PubMed=10688690;
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Pfam; PF03944; endotoxin C; 1.
Pfam; PF03945; endotoxin N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U70726; AAD10292.1; -.
                                                                                                                                                                                                                          STANDARD;
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                   --LVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLVGBLWPSGR-DPWEIFLEHVEQ 106
                                                                  LIDOKITDSVRKTALAGLOGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALBLDFV 180
                                                                                                                                                                    226
                                                                                                                                                                                                      YSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLLVLDLVALPPNYDTRTYPIBTTAQ 300
                                                                                                                                                                                                                                                                                           SRWSSTQHMYYWVGHRLNPRPIGGTLATSTQGLTMYTSINPVTLQF---TSRDVYRTESN 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Payne J.M., Fu J.M.;
Payne J.M.,
Payne J.M.,
Polleopteran-active Bacillus thuringiensis isolates and genes encodir
coleopteran-active toxins.";
Patent number US5286486. 15-FEB-1994.
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
BEPITHELIAL CELLS. OP COLEOPTERA.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the spore coat.
MISCELLANBOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
6-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry3Ab (Insecticidal delta-endotoxin CryVIIA(b)) (Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus thuringiensis (subsp. kumamotoensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=132267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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           DIGMLS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin C.
InterPro; IPR008659; endotoxin N.
InterPro; IPR008979; Gal bind like.
Pfam; PP00555; endotoxin; 1.
Pfam; PP03944; endotoxin; C; 1.
Pfam; PP03945; endotoxin C; 1.
                                                                                                                                                         DOTS-----
       GDGYVIIRDGANQTETLTFNICDD-
                                                                                                                                                                                                                                                                                                                                         (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                       1149 SETEGVFNIESVELVLEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U04368; AAA21121.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 43.2%;
es 510; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRY7AB OR CRYVIIA(B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toxin; Sporulation
SEQUENCE 1138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=HD867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q45708;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACUK
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C7AB BACUK
ID C7AB B
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563

651 622 711 682 742 829 799 889 859

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

June 21, 2004, 10:10:21; Search time 90 Seconds (without alignments) 3663.699 Million cell updates/sec

US-10-089-678-1

1 MSPNNQNEYELLDASSSTSV.......MSETEGVFNIESVELVLEEE 1167 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn1980s: *
geneseqn2000s: *
geneseqn2000s: *
geneseqn2001s: *
geneseqn2001s: *
geneseqn2003s: *
geneseqn2003bs: *
geneseqn2003bs: * A_Geneseq_29Jan04:* 1: geneseqp1980s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aau80281 Bacillus	_	Aar25997 Delta-end	Aar33768 Bt isolat	Aaw06418 Antiscara	Aar27343 B.thuring	Aar44208 Bacillus	_	Aar51692 B.thuring	Aau99256 Bacillus	Aau99255 Bacillus	. •	•	Aaw84584 Amino aci	Aaw84571 Amino aci	Aaw84591 Amino aci	~	Aaw84586 Amino aci	Aaw84582 Amino aci	Aaw84593 Amino aci	_	Aaw84578 Amino aci	Amino	Aar48678 Insectici	Aaw84570 Amino aci
ΙD	AAU80281	AAR28900	AAR25997	AAR33768	AAW06418	AAR27343	AAR44208	AAR32354	AAR51692	AAU99256	AAU99255	AAW06417	AAW84581	AAW84584	AAW84571	AAW84591	AAW84575	AAW84586	AAW84582	AAW84593	AAW84588	AAW84578	AAW84576	AAR48678	AAW84570
88	2	7	~	~	7	~	7	~	~	'n	S	~	~	~	~	7	7	7	~	~	~	7	~	7	7
Length	1167	1157	1157	1157	1157	1157	1157	1149	1149	1210	1206	1169	1157	1157	1157	1157	1157	1157	1157	1157	1157	1157	1157	1157	1157
* Query Match	100.0	66.3	66.3	66.3	66.3	66.1	1.99	9.09	9.09	54.0	53.7	52.2	51.8	51.8	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7
Score	6044	4008	4007	4007	4007	3995	3994	3662.5	3662.5	3263.5	3246.5	3152	3128	3128	3126	3125	3125	3124	3124	3124	3124	3124	3124	3123	3123
Result No.	1	8	m	4	'n	φ	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

	Aaw84569 Amino aci	Aaw84568 Amino aci	Aab82178 Cry9C #1.	Aaw84583 Amino aci	Aaw84592 Amino aci	2 Amino	Aaw84577 Amino aci	Aaw84590 Amino aci	Aaw84579 Amino aci	-	Aaw84587 Amino aci	Aaw84573 Amino aci	Aaw84567 Amino aci	Aaw84585 Amino aci	-		Aaw46857 Bacillus	Aay24960 Bacillus	Aau02034 B. thurin
AAW84566	AAM84569	AAW84568	AAB82178	AAW84583	AAW84592	AAW84572	AAW84577	AAW84590	AAW84579	AAW84589	AAM84587	AAW84573	AAW84567	AAW84585	AAW84580	AAW84574	AAW46857	AAY24960	AAU02034
~	~	8	4	N	~	~	~	7	~	N	~	~	~	~	~	~	~	~	₹"
1157	1157	1157	1157	1157	1157	1157	1157	1157	1157	1157	1157	1157	1157	1157	1157	1157	1156	1156	1156
51.7	51.7	51.7	51.7	51.7	51.7	51.6	51.6	51.6	51.6	51.6	51.6	51.6	51.5	51.5	51.5	51.4	51.3	51.3	51.3
3123	3123	3123	3123	3122	3122	3121	3121	3120	3120	3119	3118	3117	3115	3115	3114	3109	3100.5	3100.5	3100.5
56	27	28	29	30	31	32	33	34	32	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

```
Bacillus thuringiensis insecticidal protein.
                                              Insecticide; transgenic; Coleoptera larvae.
     AAU80281 standard, protein; 1167 AA
                                                                                                    03-AUG-2000; 2000JP-00236140.
                                                                                         03-AUG-2000; 2000JP-00236140.
                          30-JUL-2002 (first entry)
                                                                                                               (SDSB-) SDS BIOTECH CORP.
                                                          Bacillus thuringiensis.
                                                                    JP2002045186-A.
                                                                               12-PBB-2002.
               AAU80281;
AAU8028
```

WPI; 2002-356468/39.

A protein having insecticidal activity, a DNA encoding said protein, and an agent and a method for preventing harmful organisms.

Claim 1; Page 9-12; 19pp; Japanese.

This invention relates to a crystalline protein comprising a fully defined sequence and the nucleotide sequence encoding this protein. The defined sequence and the nucleotide sequence encoding this protein. The protein of the invention is an agent for preventing harmful organisms comprising Bacillus thuringiensis serovar galleriae SDS502, its mutant or a microbe transformed by a DNA encoding the protein. This microbe can be used to produce a protein containing the protein, or containing a protein can enact a microbe a microbe which is transformed by using the above transformed microbe, a microbe which is transformed by using the above on a seed transformed by using the above DNA, and Bacillus thuringiensis serovar galleriae SDS502 producing a protein comprising and producing a serovar galleriae SDS502 producing a protein comprising and producing a protein showing insecticidal activity. The protein of the invention may have insecticidal activity. The agent is used for preventing Coleoptera larvae. This sequence represents the Bacillus thuringiensis insecticide contains and producing a protein of the invention

Sequence 1167 AA;

```
Gene sequences encoding a toxin which is active against acarides and is obtainable from B. thuringiensis isolates PS17a, PS17b, 33f2, PS52A1, PS69D1, PS8AA1 and PS50C are given in AAQ10803-07 and AAQ10802-21 respectively. The toxin is a delta-endotoxin active against acarid pests, including the Two Spotted Spider mite. The isolates can be used against non-phytophagus mites such as acarid pests of livestock, fowl and stored prods. The genes can be cloned and used to transform other hosts, which can be used to control mites, or in the case of transgenic plants, be resistant to mites. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETFISSSTVQTGIGIVGQVLGALGVPFAGQIASPYSFIVGQL#PSSTVSVWEMIMKQVBD 120
1081 YRYVLRVTARKBGVGDGYVIIRDGANQTETLIFNICDDDTGVLSADQTSYITKTVEFTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YRYVLRVTARKEGVGDGYVI IRDGANQTBTLTFNI CDDDTGVLSADQTSYITKTVBFTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSPNNQNEYR1LDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Bacillus thuringiensis isolates and toxins - used for controlling acarid pests of livestock, fowl, stored prods. and plants.
                                                                                                                                                                                                                                                                                                 mite; phytophagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 66.3%; Score 4008; DB 2; Length 1157;
Best Local Similarity 66.1%; Pred. No. 1.7e-255;
Matches 773; Conservative 144; Mismatches 238; Indels 14;
                                                                                                                                                                                                                                                                                                 Spotted Spider;
                                                                                                                                                                                                                                                                                                                       Bacillus thuringiensis; kumamotoensis PS50C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 + 49-51; 62pp; English
                                                                                          Ä
                                                                                                                                                                              AAR28900 standard; protein; 1157
                                                                                                                                                                                                                                                                                                Endotoxin; acarides; pest; Two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bagley
                                                                                                                                                                                                                                                                                                                                                                                                                   91US-00693210.
91US-00759248.
91US-00768141.
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                                                                                                                                                                                                                            (revised)
(revised)
(first entry)
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Best Local Similarity
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13-SEP-1991;
30-SEP-1991;
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25-MAR-2003
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                                                                       LIDQKITDSVRKTALAGIQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALBLDFV
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100.0%; Score 6044;
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Matches 1167; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                               NEKRMLWDAVKEAKRLVQARNLLQDTGFNRINGENGWTGSTGIEVAEGDVLFKDRSLRLT 778
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                                                                       AKIPSFAISGOEVPLLSVYAQAANLHLILLRDASIFGAEWGFTPGEISTFYDRQVTRTAQ 240
                                                                                                                            241 YSDYCVKWYKIGLDKIKKGITISKSWLNYHQPRREMTLIVLDLVALPPNYDTHMYPIETTAQ 300
                                                                                                                                                                                                  LPLANNTEYLEYWYGHSIKYKNT-NASSALERNYGTITSNKIKYYDLANKDIFQVRSLGAD 419
                                                                                                                                                                                                                                          LANYYAQVYGVPYASFTLLDKNYGSGSVGGPTYSKPHTTMQVCTQNYNTIDEIPPENE-P 478
                                                                                                                                                                                                                                                      LSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVYSDKITQIPVVKAH 538
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LIDOKITDSVRKTALAGLÇGLGDGLDVYQKSLKNWLBNRNDTRARSVVVTQYIALELDFV 180
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                                                                                          SSIPSFAVSGHEVILLLAVYAQAVNIHILLIRDASIPGEEWGFTPGEISRFYNRQVQLTAE
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                                           PSTEQUWIDMSETEGUPNIESVELVLEEE 1167
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The sequence given is an approx. 130 kD protien known as Bacillus thuringiensis PSSOC (B.t.PSSOC). This novel delta-endotoxin has been shown to be active against the Colorado potato beetle (Leptinotarsa decemlineata). The gene encoding this toxin can be transformed into suitable hosts such as Pseudomonas, which can then be applied to the environment of coleopteran insects where they will proliferate and be ingested by the insects. This DNA sequence can be inserted into an expression vector which contains a promoter/operator region, a ribosome binding site, polyadenylation signals, etc. This will allow transcription and translation of the cells in the appropriate host. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New insecticidal Bacillus thuringiensis strain NRRL B-18746 - and DNA encoding it, vectors and transformed cells, effective against
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                                                                                                                                                                                                                                                                                                                                                                                                   potato beetle; Leptinotarsa decemlineata;
1129 PYTDQMWIEISETEGFFYIESVELIVDVE 1157
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                                                                                                                                         AAR25997 standard; protein; 1157
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                                                                                                                                                                                                                                                          (revised)
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27-JAN-1993
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Controlling lepidopteran pests - using compsn. of Bacillus thuringiensis strains or plants or microorganisms transformed with their toxin genes.
                                                                                                                                                                                                                                                              Claim 12; Page 22-25; 38pp; English
15-JUL-1993 (first entry)
                                                        Bacillus thuringiensis
                                                                                                                                                                                   KA, Bradfish GA
                                    Lepidopteran-active;
                                                                                                                                                               (MYCO ) MYCOGEN CORP.
                                                                                                                                                                                                      WPI; 1993-100566/12.
                                                                                                                                                                                                               N-PSDB; AAQ38653
                                                                                                                  11-SEP-1992;
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                     YSDYCVKWYKIGLDKLKGTTSKSWLNYHQPRREMTLLVLDLVALPPNYDTHMYPIETTAQ
                                               LTREVYTOPI VPNRETSGGPCRRWSLNSDISPSBVESAVIRSPHLPDILSEI BFYTTRAG
                                                                                      L.P.L.NVTEYLEYWVGHSIKYKNT - NASSALERNYGTITSNKIKYYDLANKDIFQVRSLGAD
                                                                                               LANYYAQVYGVPYAS FTLLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNT1DE1PPRNS-P
                                                                                                                                                               LSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVYSDKITQIPVVKAH
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The sequences given in AAR33768-70 represent lepidopteran-active toxins. The DNA encoding these sequences were used within a Ti or Ri plasmid, to transform plant cells. Whole plants can then be regenerated from the transformed cells. The toxin may also be produced by cloning Bacillus thuringiensis (Bt) . It may then be applied directly to the plant locus (Updated on 25-WAR-2003 to correct PN field.) (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LANYYAQVYGVPYASFTLLDKNTGSGSVGGFTYSKPHTMQVCTQNYNTIDEIPPENB-P 478
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                                                                                                                                                                         Ouery Match 66.3%; Score 4007; DB 2; Best Local Similarity 66.1%; Pred. No. 1.9e-255; Matches 773; Conservative 144; Mismatches 238;
                                                                                                                                              Sequence 1157 AA;
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standard; protein; 1157

AAR33768

AAR33768

AAR33768

(revised)

25-MAR-2003

Mon

91US-00808316. 92US-00828430. 93US-00014941.

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16-DEC-1991;
30-JAN-1992;
01-FEB-1993;
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LANYYQKAYGVPGSWPHMVKR--GTSSTTAYLYSKTHTALQGCTQVYESSDEIPLDRTVP 477
                                                     536 MLYLGGSVVQGPGFTGGDILKRTNPSILGTPAVTVNGSLSQRYRVRIRYASTTDFE-FTL
                                                                                    GAREIDTETYPTYLYQKVEEGVLKPYTRYRLAGFVGSSQGLEIYTIRHQTMRIVKAVPDD
              LSRGYSHRLSHITSYSFSKNASSPARYGNLPVPAWTHRSADVTNTVYSDKITQIPVVKAH
                      TLVSGTTVIKGPGFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLFVT
                                                                           ISGTRIYSINVNKTMNKGDDLTPNTFDLATIGTAFTFSNYSDSLTVGADSFASGGEVYVD
                                                                                                         NEKRMIWDAVKEAKRIVQARNILQDTGFNRINGENGWTGSTGIEVAEGDVLFKDRSLRLT
                                                                                                                                                                      SARBIDTETYPTYLYQQIDBSLLKPYTRYKLKGFIGSSQDLEIXLIRHRANQIVKNVPDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toxin 50C(a); scarab pest; toxin; insect; scarabaeidae; pest contro
larval stage insect; grain; tuberous crop; white grub; chafer grub;
cyclocephala; popillia.
                                                                                                                                                                                                                                                                                                                                                              PSTEQVWIDMSETEGVFNIBSVELVLEEB 1167
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PYTDQMWIBISETEGTFYIBSVELIVDVE 1157
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Bacillus thuringiensis; strain kumamotoensis

US5554534-A 10-SBP-1996 94US-00315468.

30-SEP-1994;

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The DNA encoding this sequence was isolated from the Bacillus

The DNA encoding this sequence was isolated from the Bacillus

Continuinglensis strain kumamotoensis. Insects in the family Scarabaeidae

constitute a serious pest control problem, especially when destructive

constitute a serious pest control problem, especially when destructive

constitutes a serious pest control problem, especially when destructive

clarval stage insects infest high value turf found in golf courses,

playing fields and lawns. The larvae of many species also attack grains,

cherous crops, and onnamentals. The larvae are known as white grubs, or

chafter grubs, and conmamentals. The larvae and the U.S. populations of

where they consume plant roots. In Burope and the U.S. populations of

these larvae and adults have developed resistance to chemical

insecticides such as the organochlorines and DDT. These toxin sequences,

and intact cells that are capable of expressing these proteins, can be

used to control many pests of the family scarabaeidae, such as species of

yclocephala, and Popillia. The toxins are active against larvae (present

in soil) and against adults. (Updated on 16-OCT-2003 to standardise OS

field)
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                                                                                                                                                                                       New nucleic acid encoding B.thuringiensis toxin active against scarab(s) - also related toxin and transformed microbes, effective against adult
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1 MSPANQNEYEIIDATPSTSVSSDSNRYPFANEPTDALQNAWYKDYLAKASGGENPELFGNP
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66.3%; Score 4007; DB 2; Length 11:
Best Local Similarity 66.1%; Pred. No. 1.9e-255;
Matches 773; Conservative 144; Mismatches 238; Indels
                                                      Michaels TB;
                                                                                                                                                                                                                                                                                                    Example 2; Col 21-26; 24pp; English.
                                                      ğ
                                                                                                                                                                                                                                                    their larvae.
                                                      Narva
(MYCO ) MYCOGEN CORP
                                                                                                          WPI; 1996-424659/42.
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                                                                                                                                      N-PSDB; AAT43222.
                                                      Foncerrada L,
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                       TLVSGTTVIKGPGFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLFVT
                                             ISGTRIYSINVNKTWNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGEVYVD
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                                                                                                                 The toxin can be used to control coleopteran pests, esp. soil-inhabiting coleoptera. The C-terminal Glu residue corresponds to a CAG (Gln) codon. The protein is obtained from a new isolate of Bacillus thurlengiensis
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                                                         New Bacillus thuringiensis isolate - used for preparing to transformed hosts for controlling coleoptera insect pests.
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                                                                                                                                                                                            Ouery Match 66.1%; Score 3995; DB 2; Best Local Similarity 66.0%; Pred. No. 1.2e-254; Matches 771; Conservative 145; Mismatches 239;
                                                                                              Claim 12; Page 18-20; 33pp; English.
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                                                                                              DNA encoding the insecticidal toxin can be cloned into baculo viruses ar transferred to other host microbes, preferably B. coli NN522 (pMYC 2320) NRRL B-18769, to control acaride pestes, or to plants which become resistant to the acaricide pestes. Specifically, the two-spotted spider mite (Tetranychus urticae) is controlled. (Updated on 25-MAR-2003 to
                   GAREIDTETYPTYLYQKVEEGVLKPYTRYRLRGFVGSSQGLEIYTIRHOTNRIVKAVPDD
                                                                        LLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMSSDSHAPSPHIDTGEIDLNENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Controlling acaride pests e.g. two spotted spider mite - utilising Bacillus thuringiensis delta-toxins cloned into microbe hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crystal protein; delta endotoxin; acaricide; pesticide;
biological control agent; transgenic plant; crop improvement.
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PNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDDDTGVLSADQTSYITKTVEFT 1138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Delta-endotoxin; larvae; Anomala cuprea; spore;
thuringiensis; virus; insect; FERM BP-3465.
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                                           QLTREVYTDPIVFNRETSGGFCRRWSLN----SDI-----SFSBVESAVIRSPHLPDIL
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                                                                                                                                  DIPQVRSLGADLANYYAQVYGVPYASPTLLDKNTGSGSVGGPTYSKPHTTMQVCTQNYNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This insecticidal protein has activity against Coleopteran insect larvae and has been isolated from Bacillus thuringiensis serovar japonensis strain Buibui. (Updated on 16-OCT-2003 to standardise OS field)
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/note= "amino acids 751-766 are not given in the
specification and so have been decoded from AAQ58975"
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                                                                                                                                                                               B.thuringiensis serovar Japonensis insecticidal protein.
                                                                                                                                                                                                  insecticidal protein; Coleoptera larvae; Buibui fungus
                     Bacillus thuringiensis; (serovar Japonensis strain Buibui).
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                                                                                                                                                                                                                                                                                                                                           The present invention relates to a new pesticidal polypeptide. The invention is useful for impacting an insect pest by applying the the molecules of the invention to the environment of the insect pest by spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn rootworm or southern corn rootworm or for invention is also useful for increasing insect target range and for producing transgemic microorganisms and plants that express the pesticidal polypeptide. The invention is also to produce the pesticidal polypeptide of the invention is also to produce the pesticidal polypeptide of the invention is also acid sequence represents a Bacillus thuringiensis wild-type Cryl218
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                                                                                                                                                                                                                                                                                       pest e.g.
                        Pesticidal, spraying, dusting, broadcasting, seed coating, insect pest, Colorado potato beetle, western corn rootworm; southern corn rootworm; insect target range; endotoxin; Cryl218.
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   Bacillus thuringiensis Cry1218-2 protein sequence.
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23-OCT-2001; 2001US-00032717.
                                                                                                                                            24-OCT-2001; 2001WO-US045468
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                                                                      Bacillus thuringiensis
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Best Local Similarity
Matches 667; Conserv
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                              -----TLKYNPVSK 456
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                                                                                                                                                      SKKDALQTSVTDYQVNQAANI VECLSDBLYPNBKRMLWDAVKRAKRLVQARNLLQDTGPN
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DLAN----YYAQVYGVPYASFTLLDK--NTGSGSVGGPTYSKPHTTMQVCTQNYNTID-
                                                                    -----BIPPE--NEPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRS
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                     | : | : | : | : | 415 VLLDIVFPGYTYIPFGMPEVBFFWVNQLNYTRK----
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TLTFSASDYDTNGMYNTQVSNTNGYNTNNAYNTQASSTNGYNANNMYNTQASNTNGYNTN 1160
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--TLKYNPVSK 456
                                                                                                                                                                             ALEKAGKYRVRLRYATDADIVLHVNDA----QIQMPKTWNPGBDLTSKTFKVADAITTL
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                                                                                                             574 KSPLSQRYRARIRYASTTNLRLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAF
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                                ---BIPPE--NEPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVPAWTHRS
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larval stage insect; grain; tuberous crop; white grub; chafer grub;
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415 VLLDIVYPGYTYIPPGMPBVBPPMVNQLNNTRK---
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                                                                                                           24-OCT-2001; 2001WO-US045468
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467 LELPPETSGOPNYESYSHRICHIT-FIYSSSTST----YVPVPSWTHRSADLTNTVKSG
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                               SNGAVLLDIVYPGYTYTPPGMPBTEPFMVNQLMNTRKT--LTY-KP-ASKDIIDRTRDSB
                                                                    DEIPPE--NEPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVPAWTHRSADVTNTVYSD
                                                                                                                                       KITQIPWWAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cry9C; crystal protein; toxic; mutant; insecticide; insect; transgenic plant; transgenic seed; lepidoptera.
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ESVELIVDVE 1169
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Synthetic.
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The DNA encoding this sequence was isolated from the Bacillus
The DNA encoding this sequence was isolated from the Bacillus
Thuringiensis strain kumamotoensis. Insects in the family Scarabaeidae
Constitute a serious pest control problem, especially when destructive
larval stage insects infest high value turf found in golf courses,
playing fields and lawns. The larvae of many species also attack grains,
tuberous crops, and ornamentals. The larvae are known as white grubs, or
chafer grubs, and can be found in decaying organic matter, or in the soil
where they consume plant roots. In Burope and the U.S. populations of
these larvae and adults have developed resistance to chemical neguences,
insecticides such as the organochlorines and DDT. These toxin sequences,
and intact cells that are capable of expressing these proteins, can be
cused to control many pests of the family scarabaeidae, such as species of
cyclocephala, and Popillia. The toxins are active against larvae (present
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                                                                                                                                                                                                                                                                                 New nucleic acid encoding B.thuringiensis toxin active against scarab(s) also related toxin and transformed microbes, effective against adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSPNNQNBYBILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
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Best Local Similarity 54.0%; Pred. No. 5.7e-199;
Matches 653; Conservative 179; Mismatches 294;
                                                                                                                                                                                            Michaels TE;
                                                                                                                                                                                                                                                                                                                                                    Claim 2; Col 29-36; 24pp; English.
                                                                                   91US-00808316.
92US-00828430.
93US-00014941.
                                                   94US-00315468
                                                                                                                                                                                            Poncerrada L, Narva KB,
                                                                                                                                                                                                                                                                                                                    pests and their larvae
                                                                                                                                                         (MYCO ) MYCOGEN CORP.
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                                                                                                                                                                                                                                              N-PSDB; AAT43221
                                                 30-SEP-1994;
                                                                                     16-DEC-1991;
                                                                                                                      01-FEB-1993;
                  10-SEP-1996
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                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of a Cry9C (crystal) mutant protein which is toxic to an insect species. It is modified in the method of the invention in an attempt to improve its toxicity. The improved proteins are useful for producing transgenic plants and seeds in controlling insects feeding on a plant. The transgenic plants are also useful for producing transgenic plants with similar characteristics, or for introducing the improved cry9C gene (including fragments) into the same plant variety or related plant species. The Cry9C protein can be obtained from cultured cells of the transgenic plants and used in insecticide compositions against lepidopteran insects. especially Ostrinia mubilalis, Heliothis virescens and Diatraea grandiosella. The cry9C gene can be expressed in combination with another insect control protein (e.g. Another B. thuringiensis derived crystal protein especially Cry1Ab or Cry1B-type protein), and used to transform B.thuringiensis, which crystalery of insect pests, or insects where insect resistance development is prevented or delayed. (Note: this sequence is not given in the second or protein in the sequence is not given in the second or secon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLTREVYTOPIVENRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSEIRFYTTRA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 GLPLNNTEYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKY---YDLANKDIFQVRSL 416
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                                                                                                                                                                                                                                 New Bacillus thuringiensis Cry9C crystal proteins with improved toxicity - useful for producing transgenic plants in controlling pest insects, especially Ostrinia nubilalis, Heliothis virescens and Diatraea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETFISS-STVQTGIGIVGQVLGALGVPPAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.8%; Score 3128; DB 2; Length 1.
llarity 52.4%; Pred. No. 2.2e-197;
Conservative 195; Mismatches 326; Indels
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                                                                                                                                  (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                     Example; Page; 40pp; English.
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                                                                 98WO-EP004033
                                                                                                  97US-00884389
                                                                                                                                                                                                    WPI; 1999-105666/09.
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nes 620; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1157 AA;
                                                                                                                                                                                                                                                                                   grandiosella.
                                                                   25-JUN-1998;
                                                                                                  27-JUN-1997;
   WO9900407-A2
                                  07-JAN-1999
                                                                                                                                                                   De Roeck S,
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1065 PNWNSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLIFNICDDDTGVLS 1124 1005 IPCHAYTSFTELTWRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI 1064 764 PHIDTGEIDLMENTGIWVVPKIPTINGYATLGNLELVEEGPLSGETLERAQQQEQQWQDK 944 HHHKVHLVRAVPDNLVSDTYSDGSCSGINRCDBQHQVDMQLDAEHHPMDCCEAAQTHBFS 414 AVDFASALIGIYGVARASFVPGGLFNGTISPANGG------CRDLYDTNDELPP NLVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRING--ENGWTGSTGIBVA RHRANGIVKNVPDNLLPDVLPVNSCGGIDRCSBQQYVDANLALENNGENGNMSSDSHAPS MARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSI PYVYNDALPE GADLANYYAQVYGVPYASFTL - - LDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTIDEIPP ENEPLSRGYS-HRLSHITSYSPSKN-ASSPARYGNLPVFAWTHRSADVTNTVYSDKITQI PVVKAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTN 593 LRLFVTISGTRIYSINVNKTMNKGDDLTFNTF---DLATIG---TAFTFSNYSDSLTVGA DSPASGGEVYVDKFEL1 PVNATPEAEEDLDVAKKAVNGLFTSKKDALQTSVTDYQVNQAA **EGDVLPKDRSLRLTSARBIDTBTYPTYLYQIDBSLLKPYTRYKLKGFIGSSQDLBIKLI** Cry9C; crystal protein; toxic; mutant; insecticide; insect; transgenic plant; transgenic seed; lepidoptera. Amino acid sequence of Bacillus thuringiensis Cry9C mutant Ź AAW84584 standard; protein; 1157

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                                                                                                                                              New Bacillus thuringlensis Cry9C crystal proteins with improved toxicity
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                                                                      (PLBZ ) PLANT GENETIC SYSTEMS
                        98WO-EP004033
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1005 IPCHAYTSPTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI 1064
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                           AVDFRSALAGIYGVNRASFVPGGLFNGTTSPANGG------CRDLYDTNDBLPP
                                                                                                                       NLVECLSDELYPNEKRALMDAVKEAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVA
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GADLANYYAQVYGVPYASFTL--LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP
                                                                                            ENEPLSRGYS-HRISHITSYSPSKN-ASSPARYGNLPVPAWTHRSADVTNTVYSDKITQI
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Synthetic.
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This is the amino acid sequence of a Cry9C (crystal) mutant protein which is toxic to an insect species. It is modified in the method of the invention in an attempt to improve its toxicity. The improved proteins are useful for producing transgenic plants and seeds in controlling insects feeding on a plant. The transgenic plants are also useful for producing more transgenic plants with similar characteristics, or for introducing the improved cry9C gene (including fragments) into the same plant variety or related plant species. The Cry9C protein can be obtained from cultured cells of the transgenic plants and used in insecticide compositions against lepidopteran insects, especially Ostrinia mubilalis, Heliothis virescens and Diatraea grandiosella. The cry9C gene can be expressed in combination with another insect control protein (e.g. crypsessed in combination with another insect control protein (e.g. cry1B-type protein), and used to transform B.thuringiensis, which produces other insecticidal toxins. Such strains are useful against a produces other insecticidal toxins. Such strains are useful against a variety of insect pests, or insects where insect resistance development is prevented or delayed. (Noce: this sequence is not given in the second or delayed. (Noce: this sequence is not given in the constinct in the second or delayed in the information provided by the
                                                                                                                                                                                                              New Bacillus thuringiensis Cry9C crystal proteins with improved toxicity - useful for producing transgenic plants in controlling pest insects, especially Ostrinia nubilalis, Heliothis virescens and Diatraea grandiosella.
                                                                                                (PLBZ ) PLANT GENETIC SYSTEMS NV
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98WO-EP004033
                                               97US-00884389
                                                                                                                                               Van Rie J;
                                                                                                                                                                                                 WPI; 1999-105666/09
25-JUN-1998;
                                               27-JUN-1997;
                                                                                                                                                  Roeck S,
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Sequence 1157 AA;

240 119 61 SLSISGRDAVQTALTVVGRILGALGVPPSGQIVSFYQPLLATIMPVNDTAIWEAFWRQVB 120 - FPV-SSNFMDYWSGHTLRRSYLNDSAVQEDSYGLITTTRATINPGVDGTNR----IEST 413 OYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLLVLDLVALFPNYDTRTYPIETTA 299 QLTREVYTDPIVFNRETSGGFCRRWSLNSDISPSEVESAVIRSPHLPDILSBIEFYTTRA 359 360 GLPLANTEYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKY---YDLANKDIPQVRSL 416 417 GADLANYYAQVYGVPYASFTL--LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDEIPP 474 9 61 ETFISS-STVQTGIGIVGQVLGALGVPFAGQIASPYSFIVGQLMPSSTVSVWEMIMKQVE VAKI PSFAI SGOEVPLLSVYAQAANLHLLLLRDAS I FGAEWGFTPGEI STFYDRQVTRTA 1 MSPNNONEYEILDASSSTSVSDNSVRYPLANDOTTTLONMNYKDYLRMSEGENPELFGNP Gaps 42; Match 51.7%; Score 3126; DB 2; Length 1157; Local Similarity 52.3%; Pred. No. 2.9e-197; les 619; Conservative 195; Mismatches 327; Indels 42. 241 120 121 240 300 301 Query Match 360 Best Loca Matches g 쉱 셤 셤 g ð 8 કે ઠે Š 용 ઠે g ò

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MARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPE 1004 1005 IPGWNYTSPTELTWRLQQAMNLYDLRNAIPNGDFRWGLSDWNATSDVNVQQLSDTSVLVI 1064 1065 PNWASQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDDDTGVLS 1124 SHWDAQVSQQLRVNPNCKYVLRVTARKVGGGGGYVTIRDGAHHQETLTFNACDYDVNGTY 1114 638 874 592 578 646 706 698 764 824 814 884 PHIDTGEIDLMENTGIWVVFKIPTTNGYATLGMLELVEEGPLSGETLERAQQQEQQWQDK 944 875 SYINTGDLNASVDQGIWVVLKVRTTDGYATLGNLELVEVGPLSGESLERBQRDNAKWNAE 934 461 DE---STGSSTHRLSHVIFFSPOTNQAGSIANAGSVPTVWTRRDVDLNNTITPNRITQL -- CRDLYDTNDELPP PVVKAHTLVSGTTVI KGPGFTGGNI LKRTSSGPLAYTSVSVKSPLSQRYRARI RYASTTN 593 LRLPVTISGTRIYSINVNKTMNKGDDLTFNTF---DLATIG---TAFTFSNYSDSLTVGA DSFASGGEVYVDKFELIPVNATFEABEDLDVAKKAVNGLPTSKXDALQTSVTDYQVNQAA NLVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVA RHRANGIVINVPDNILLPDVLPVNSCGIDRCSBQQYVDANLALENNGENGNMSSDSHAFS ENEPLSRGYS-HRLSHITSYSPSKN-ASSPARYGNLPVPANTHRSADVTNTVYSDKITQI RCDVLPKDRSLRLTSARBIDTETYPTYLYQQIDESLLKPYTRYKLKGFIGSSQDLBIKLI 1125 ADQTSYITKTVBFTPSTEQVWIDMSETEGVFNIESVELVLEBE 1167 414 AVDFRSALIGIYGVNRASFVPGGLFNGTTSPANGG--462 533 519 647 639 707 669 765 759 825 945 475 셤 ઠે 셤 ઠે 셤 ò 8 ठे 셤 ò 셤 δ d ሯ 셤 ð 셤 ð 8 6 કે ద ŝ 셤

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June 21, 2004, 10:12:40; Search time 402 Seconds (without alignments) 819.552 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/PCT_MRW PUB_pep:*
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| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 1, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 72, Appl	28,	Sequence 6, Appli	Sequence 74, Appl	Sequence 76, Appl	Sequence 7, Appli	Seguence 63, Appl	Sequence 23, Appl
	ID	US-10-089-678-1	US-10-032-717-4	US-10-414-637-4	US-10-606-320-4	US-10-032-717-2	US-10-414-637-2	US-10-606-320-2	US-10-099-285-72	US-10-428-961-28	US-10-614-524-6	US-10-099-285-74	US-10-099-285-76	US-09-988-462-7	US-10-428-961-63	US-09-826-660-23
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	Query Match Length DB	1167	1210	1210	1210	1206	1206	1206	1156	1156	1152	1150	1134	1207	1227	1186
de	Query Match	100.0	54.0	54.0	54.0	53.7	53.7	53.7	51.3	51.3	47.7	46.7	44.8	41.7	40.7	40.6
	Score	6044	3263.5	3263.5	3263.5	3246.5	3246.5	3246.5	3100.5	3100.5	2884.5	2825.5	2710	2519.5	2457	2454.5
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16 2449.5 40.5 17 2446.5 10.5 18 2230.5 36.9 22 2230.5 36.9 22 2230.5 36.9 22 2230.5 36.9 23 2230.5 36.9 24 2230.5 36.9 25 2230.5 36.9 26 2230.5 36.9 27 2230.5 36.9 28 2230.5 36.9 39 2229.5 36.9 39 2229.5 36.9 39 2229.5 36.9 39 2229.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 39 2225.5 36.9 30 2225.5 36.9 31 2229.5 36.9 31 2229.5 36.9 32 2227.5 36.9 34 2227.5 36.9 36.9 37 2225.5 36.9 38 2227.5 36.9 39 2227.5 36.9 30 2227.5 36.9 3	Match ocal Simi s 1167;	MSPNI
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APPLICANT: Andre R. Duck
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APPLICANT: Nicholas B. Duck
APPLICANT: Riang Feng
APPLICANT: Ronald D. Plannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Eahn
TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
TITLE OP INVENTION: Pesticidal Activity Against Coleopterans
FILE REPERBNCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
FRIOR APPLICATION NUMBER: 60/242,838
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                  61 ETPIS-SSTVQTGIGIVGQVLGALGVPPAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVE
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                           181 AKIPSFAISGQEVPLLSVYAQAANLHLLLLRDASIPGAEWGFTPGEISTFYDRQVTRTAQ
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                                                                              241 YSDYCVKMYNTGLDKLKGTNAASWLKYHQFRREMTLLVLDLVALFPWYDTRTYPIETTAQ
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RESULT 2 US-10-032-717-4 ; Sequence 4, Application US/10032717

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1108 TETLTENICDDDT-GVLSA	Application US/10606320 No. US20040091505A1 No. SAMATION: Ander R. Abad Ronald D. Flannagan Rafael Herrmann	APPLICANT: Intecoder W. Kann APPLICANT: Albert L. Lu APPLICANT: Billy Fred McCutchen APPLICANT: James R. Presnail APPLICANT: James R. Presnail APPLICANT: Cao-Guo Yu APPLICANT: Cao-Guo Yu TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal APPLICANT: Applicant Cao-Guo Yu TITLE OF INVENTION: Activity FILE REFERENCE: 35718/263948	CURRENT APPLICATION NUMBER: 0'5/10/606,320 CURRENT PILING DATE: 2003-6-5.35 FRIOR APPLICATION NUMBER: 60/391,786 PRIOR APPLICATION NUMBER: 60/460,787 PRIOR APPLICATION NUMBER: 60/460,787 PRIOR PILING DATE: 2003-04-04 NUMBER OF SEQ ID NOS: 134 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID SEQ ID NOS: 130 LENGTH: 1210 TYPE: PRT	ore 3263.5; DB 16; Length 1210; ed. No. 3e-258; Mismatches 284; Indels 119; Gaps 21; NSVRYPLANDQTTILQNMNYKDYLRMSBGENPELFGNP 60 :	0) 1 0) 44 0

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1101 TLTFSASDYDTNGMYNTQVSNTNGYNTNNAYNTQASSTNGYNANNMYNTQASNTNGYNTN 1160
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| PUBLICANT: Andre R. Abad
| APPLICANT: Andre R. Abad
| APPLICANT: Andre R. Buck
| APPLICANT: Alang Peng
| APPLICANT: Alang Peng
| APPLICANT: Theodore W. Rahn
| APPLICANT: Theodore W. Rahn
| APPLICANT: Lynn B. Sims
| APPLICANT: Lynn B. Sims
| TITLE OF INVENTION: Genes Encoding No. USZUD30177528A1el Proteins With
| TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
| FILE OF INVENTION: Pesticidal Activity Against Coleopterans
| TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
| FILE OF INVENTION: UNUBER: US/10/414,637
| CURRENT APPLICATION NUMBER: US/10/032,717
| PRIOR APPLICATION NUMBER: 60/242,838
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                                                                                           990 LVQSIPYVYNDALPRIPGMNYTSPTELTNRLQQAMNLYDLRNAIPNGDFRNGLSDWNATS
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                                   930 TLERAQQQEQQWQDIQMARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQN
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Best Local Similarity 53.4%; Pred. No. 7.5e-257;
Matches 665; Conservative 172; Mismatches 290; Indels 119;
                                                                                                                                                                                                                                                                                                                                        ----DOTSYITKTVEFTPSTEGVWIDMSETEGVFNIESVELVLEEB 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/10414637; Publication No. US20030177528A1
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                                                                                                                                                                                        Gaps
                                                                                                                                                         DB 13; Length 1206;
                                                                                                                                                        Query Match 53.7%; Score 3246.5; DB 13; Length 1206
Best Local Similarity 53.4%; Pred. No. 7.5e-257;
Matches 665; Conservative 172; Mismatches 290; Indela 119;
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                      ; ORGANISM: Bacillus thuringiensis US-10-032-717-2
                                                                                 LENGTH: 1206
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Length 1206;

APPLICANT: Ronald D. Flannagan
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: Albert E. Lu
APPLICANT: James K. Presnail
APPLICANT: James P.H. Wong
APPLICANT: Cao-Guo Yu
ITILE OP INVENTION: Genes Encoding Proteins With Pesticidal
ITILE OP INVENTION: Activity
ITILE OP INVENTION: Activity
ITILE OP INVENTION Activity
FILE REPERCES: 33718/263948
CURRENT PILING DATE: 2003-06-25
PRIOR APPLICATION NUMBER: 60/31,786
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR PILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 134
SOSTWARE: PastSEQ for Windows Version 4.0

SOFTWARE: FastS SEQ ID NO 2 LENGTH: 1206

TYPE: PRT

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TLTFNICDDDT-GVLSA------ 1125
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| : | : | | : | : | | 415 ULLDIVYPGYTYIPPGMPEVERPMVNQLANTRK-------TLKYNPVSK
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                                                                                      360 GLPLNNTEYLEYWVGHSIKYKNTNASSALERNYGTITS-NKIKYYDLANKDIPQVRSLGA
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                                                                                  1 MSPNNQNBYRILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPBLFGNP
                                                             Gaps
                                    Length 1206;
                                    53.7%; Score 3246.5; DB 16; Length 1206 ilarity 53.4%; Pred. No. 7.5e-257; Conservative 172; Mismatches 290; Indels 119;
; ORGANISM: Bacillus thuringiensis
US-10-606-320-2
                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSPNNQNBYBILDASSSTSVSDNSVRYPLANDQTTTTQNMNYKDYLRMSBGBNPELPGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLIDOKITDSVRXTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALBLDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VNAIPLFAVNGQQVPLLSVYAQAVNLHILLLKDASLFGBGWGFTQGBISTYYDRQLBTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GADLANYYAQVYGVPYASFTL--LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDEIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGT-----APTFSNYSDSLTVGAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Length 1156;
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Best Local Similarity 52.0%; Pred. No. 6.9e-245;
Matches 615; Conservative 196; Mismatches 330; Indels
OR APPLICATION DATA:
APPLICATION NUMBER: 09/002,285
FILING DATE: cUnchrown>
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-UUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-UUL-1996
                                                                                                                                                                   REFERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ 1D NO: 72:
US-10-099-285-72
                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
                                                                                                                                                                                                                                      INPORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 amino acids
                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
     PRIOR
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                                                     ---TPSNYSDSLTVGADSPAS-GGEVYVDKFELIPVNATFEAEEDLDVAKKAVNGLFTSK 689
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                                                                       KGPI GSSQDLEIKLI RHRANQI VKNVPDNLLPDVLPVNSCGGI DRCSEQOYVDANLALEN
                                                                                                                                                                                                                                                                                                                             870 NGENGNMSSDSHAFSFHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVEEGPLSGB
                                                                                                                                                                                      NGENGWIGSTGIBVARGDVLPKORSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 72, Application US/10099285
Publication No. US20030105319A1
GENERAL INFORMATION:
MICKET, Carol
Marva, Kenneth R.
Marva, Kenneth R.
Malor, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION:
MUNBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Plorida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285
APPLICATION THE CONTROL CLASSIFICATION: CURROWN>
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
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                                         301 QLTREVYTDPIVPNPPANVGLCRRÆGTNPYNTPSELENAFIRPPHLFDRLNSLTISSNR- 359
                                                                                                                                                                                                                                                      360 GLPLANTEYLEYWVCHSIKYKATNASSALERNYGTITSNKIKY---YDLANKDIFQVRSL 416
                                                                                                                                                                                                                                                                         OLTREVYTOPIVENRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSEIBFYTTRA 359
61 SLSISGRDAVQTALTVVGRILGALGVPFSGQIVSFYQFLLNTLWPVNDTAIWEAFMRQVB 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417 GADLANYYAQVYGVPYASFTL--LDKWTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP
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                                                                                                                                         OYSDYCVKWYNTGLDKLKGTNAASWLKYHOPRREMTLLVLDLVALFPNYDTRTYPIBTTA
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                             120 DLIDQKITDSVRKTALAGLØGLØDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOTSYLTKTVEPTPSTEOVWIDMSETEGVFNIESVELVLEER 1167
                                                                                                                                           240
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APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Amy J.
APPLICANT: Rupar, Mark J.
TITLE OF INVENTION: Lebymoteotides, Compositions, and Methods of Use (Amended)
FILE REFERENCE: MECOZ01--1
CURRENT APPLICATION NUMBER: US/10/428,961
CURRENT PILING DATE: 2000-09-13
FRIOR APPLICATION NUMBER: 09/661,322
FRIOR APPLICATION NUMBER: 60/153,995
FRIOR APPLICATION NUMBER: 60/153,995
FRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTING DATE: 1999-09-15
SEQ ID NO 28
LENGTH: 1156
                                                                                                                                                                                                                                                                       ARKRGASEKAYYAAKQAIDRLPADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPEI 1005
                                                                                                                                                                                                                                                                                                                              PGMNYTSFTELTWRLQQAMNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIP 1065
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 766 GDVLFKDRSLRLTSARBIDTRTYPTYLYQQIDESLLKPYTRYKLKGFIGSSQDLRIKLIR 825
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                                                         GGPFFKGRALQLASAR----ENYPTY1YQKVDASVLKPYTRYRLDGFVKSSQDLEIDLIH
                                                                                                                                                           HRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMSSDSHAFSF
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                                          LVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVAE
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.larity 52.0%; Pred. No. 6.9e-245;
Conservative 196; Mismatches 330; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1126 DQTSYITKTVEFTPSTEQVWIDMSRTEGVFNIESVELVLERE 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 28, Application US/10428961
Publication No. US20030237111A1
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus thuringiensis
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Matches 615; Conserv
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US-10-428-961-28
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1012 SFTELTURLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIPNWNSQV 1071
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                                                                                            ELYPNEKRMLWDAVKBAKRLVQARNILQDTGFNRING--ENGWTGSTGIEVAEGDVLFKD 772
                                                                                                                                                                       892 IDLANENTGIWVVFKIPTINGYATLGNLELVEEGPLSGETLERAQQQEQQWQDKMARKRGA 951
                                                                                                                                                                                                                                                                                                                                                                                                     KNYPDNILLPDVLPVNSCGGIDRCSROOYVDANLALENNGB-NGNMSSDSHAPSPHIDTGB
                                                                                                                                                                                                                                                                                                                            773 RSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGPIGSSQDLEIKLIRHRANQIV
                                                                                                                                                                                                                                                   VYVDKFELI PVNATPRAEEDLDVAKKAVNGLFTSKKDALQTSVTDYQVNQAANLVECLSD
LFVTISGTRIYSINVNKTWNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Schnepf, H. Ernest
Wicker, Carol
Narva, Kenneth B.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, iloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Plorida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKTVEPTPSTEOVWIDMSETEGVFNIESVELVLEEE 1167
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APPLICATION NUMBER: US/10/099,285
FILING DATE: 15-Mar-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/002,285
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 74, Application US/10099285; Publication No. US20030105319A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 VAKIPSFAI----SGQEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLLVLDLVALFPNYDTRTYFI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 ETTAQLIREVYIDPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSEIRFY 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 TTRAGLPLNNTBYLEYWGHSIKYKNTNASSALERNYGTITSNKIKYYDLANKDIFQVRS 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416 LGADLANYYAQVYGVPYASFTLLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDEIPPE 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                          APPLICANT: Arnaut, Greta
APPLICANT: Boets, Annemie
APPLICANT: Boets, Annemie
APPLICANT: Damme, Nicole
APPLICANT: Damme, Nicole
APPLICANT: Wathieu, Eva
APPLICANT: Wanneste, Stijn
APPLICANT: Vanneste, Stijn
FILE REFERRENCE: NEWBER: US/06/14,524
CURRENT APPLICATION NUMBER: US/09/739,243
PRIOR APPLICATION NUMBER: 60/173387
PRIOR PLING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

47.7%; Score 2884.5; DB 15; Length 1152;
Best Local Similarity 49.1%; Pred. No. 3.8e-227;
Matches 578; Conservative 200; Mismatches 365; Indels 33;
                                                                         ; Sequence 6, Application US/10614524; Publication No. US20040016020A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1152
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                                                                                                                                                                                                                                                                          47;
                                                                                                                                                                                                                                                                          364; Indels
                                                                                                                                                                                                                                                  Query Match
46.7%; Score 2825.5; DB 14
Best Local Similarity 48.6%; Pred. No. 2.6e-222;
Matches 574; Conservative 197; Mismatches 364;
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1.-UUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1.-UUL-1996
ATTORNEY/AGENT INFORMATION:
                                                       NAME: SANGER, JAY M.
REGISTRATION NUMBER: 39,355
REPERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEFRAT (352) 375-8100
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 TOPOLOGY: linear
NOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-10-099-285-74
                                                                                                                                                      LENGTH: 1150 amino acids
                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
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PGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIP 1065
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                                                                                                                                                                                                             GGPFFKGRALQLASAR----ENYPTYIYQKVDASTLKPYTRYKLDGFVQSSQDLBIDLIH 808
                                                                                                                                                                                                                                                                               886 HIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVBEGPLSGETLERAQQQEQQWQDKM 945
                                                                                                                                                                                                                                                                                                     GDVLFKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFIGSSQDLBIKLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NWNSQVSQQPTVQPMYRYVLRVTARKEGVGDGYVI IRDGANQTBTLTFNI CDDDTGVLSA
                        HRANQI VKNVPDNLLPDVLPVNSCGGI DRCSEQQYVDANLALENNGENGNMSSDSHAFSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1126 DOTSYITKTVEPTPSTEQUWIDMSETEGVFNIESVELVLEER 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wicker, Carol
Narva, Kenneth B.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/886,615
PILING DATE: 1-UUJ-1997
APPLICATION NUMBER: US 08/674,002
PILING DATE: 1-UUJ-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285
PLING DATE: 15-Mar-2002
CLASSIFICATION: «UNKIDOMI»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/002,285
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 76, Application US/10099285
Publication No: US20030105319A1
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Gainesville
STATE: Florida
COUNTRY: USA
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VTARKEGVGDGYVIIRDGANQTETLIFNICDDDTGVLSADQTSYIIKTVEFTPSTEQVWI 1146
                                                           SCSGINRCQEQQAVNAQLETERHHPMDCCEAAQTHEPSSYIDTGDLNSSVDGGIWAIFKV
                                                                                                                       PADYODOKLINSGVEMSDMLAAQNLVQSI PYVYNDALPEI PGMNYTSPTELTNRLQQAMNL
                                                                                                                                                                                                    SCGGIDRCSEQQYVDANLALENNGE-NGNMSSDSHAPSPHIDTGBIDLNENTGIWVVPKI
                                                                                                                                                                                   YDLRNA I PNGDFRNGLSDWNATSDVNVQQLSDTSVLVI PNWNSQVSQQFTVQPNYRYVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-No. US20030046726A1-2001
CLASSIPICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSER: Syngenta Biotechnology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meige, J. Timothy
REGISTRATION NUMBER: 38,241
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1114 BVNBTEGAFHIDSIEFVBTEK 1134
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09988462; Publication No. US20030046726A1
GENERAL INFORMATION:
March Coriel, Michael G.
Fewis, Relly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Blis J.
Merlin, Blis J.
Leaulis, Raten L.
                                                                                                                                                                                                                                                                                                       DMSETEGVFNIESVELVLEER 1167
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ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-09-988-462-7
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                                                                                                                                                                                                    Length 1134;
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                                                                                                                                                                                                 Query Match 44.8%; Score 2710; DB 14; Best Local Similarity 48.1%; Pred. No. 7.9e-213; Matches 559; Conservative 195; Mismatches 345;
                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-10-099-285-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
                                                                           LENGTH: 1134 amino acids
                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                           INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
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ORGANISM: Bacillus thuringiensis
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                                                                                                                                                                                                             LVLDLVALPPNYDTRTYPIETTAQLTREVYTDPIVFNRETSGGFCRRWSLNSDISPSEVE 336
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                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR EQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
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KESULY 14

US-10-428-961-63

Sequence 63, Application US/10428961

Sequence 63, Application Wol10428961

Sequence 63, Application Wol10428961

Sequence 63, Application Wol10428961

Sequence 63, Application Wol2003237111A1

GENERAL INFORMATION:

APPLICANT: Chu, Chib.Rei

APPLICANT: Glimer, Amy J.

APPLICANT: Rupar, Mark J.

TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

TITLE REPRENCE: MECO201-1

CURRENT FILING DATE: 2003-05-02

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

WUMBER OF SEQ ID NOS: 63

SOFTWARE: Patent In version 3.2

SEQ ID NO 63:

SEQ ID NO 63:
                                                                                                                                                                                                                                                                                                                                                                                                            1080
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                                                                                                                                                                                                                                           QAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPBIPGMYTSFTELTNRL
                                                                                                                                                                                                                                                                                                        LIDOKITDSVRKTALAGIÇGIGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFV
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                                                                                  WVVPKI PITNGYATLGNLELVBEGPLSGETLERAQQQEQQWQDKMARKRGASEKAYYAAK
813 VESPIGRCGEPNRCA--PHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDVGCTDLHENLGV
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LTREVYTDPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSBIEFYTTRAG 360
                                                                 LPLNNTEYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKYYDLANKDIFQVRSLGADL 420
                                                                          405 ILLITTPVNGVPWARRWW--RNPLNSLRGSLLYTIGYT--GVGTQLFDSETELPPETTERP 460
                                                                                                                                                                 KAHTLVSGTTVIKGPGFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTNLRL 595
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                                                                                                                                 LSRGYSHRLSHITSYSFSKNASSPARYGN---LPVFAWTHRSADVTNTVYSDKITQIPVV
                                                                                                                                          161 NYESYSHRLSNIRLIS------GNTLRAPVYSWTHRSADRIWIISSDSITQIPLV
                                                                                                                                                                                                                                  656 YVDKFBLIPVNATFEARBDLDVAKKAVNGLFTSKKD-ALQTSVTDYQVNQAANLVBCLSD
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48 DPFVSASTVQTGINIAGRILGVLGVPRAGQIASFYSFLVGELWPRGR-DPWEIFLEHVBQ 106
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                                                                                                                                                     Encoding Pesticidal Toxins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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                                  GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cardineau, Guy A.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Narva, Kenneth B.
TITLE OF INVENTION: Plant-Optimized Genes Enc FILE REFERENCE: MA-714XC2D1
CURRENT APPLICATION NUMBER: US/09/826,660
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/178,252
PRIOR APPLICATION NUMBER: 60/055,215
PRIOR APPLICATION NUMBER: 60/055,215
PRIOR APPLICATION NUMBER: 60/055,215
PRIOR APPLICATION NUMBER: 60/056,445
PRIOR APPLICATION NUMBER: 60/076,445
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTL VEY: 2.0
     US/09826660
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; Sequence 23, Application U.; Patent No. US20010026940A1
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                                                                                                                                                                                                                                                                 963 PEBLECRIFTAFSLYDARNVIKNGDFNNGLSCMAVKGHVDVEEQNNHRSVLVVPEWEAEV 1022
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                                  833 KNVPDNLLPDVLPVNSCGCIDRCSEQQYVDANLALENNGENGNMSSDSHAPSFHIDTGEI 892
                                                                                                                                                          DIANENTGIWAVPKI PTTNGYATLGNLELVEEGPLSGETLERAQQQEQQWQDKWARKRGAS 952
596 FVIISGTRIYSINVNKTMAKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGEV 655
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Search completed: June 21, 2004, 10:23:47 Job time: 417 secs

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PSOURNCE FROM N.A.

SEQUENCE FROM N.A.

A SEAND S., Yamamoto T.;
A Asano S., Yamamoto T.;
A Basano S., Yamamoto T.;
B MGG-20015070; Ficzin EMBL/GenBank/DDBJ databases.
B MGG-20015070; Ficzin activity; IEA.
G GG-0005952; Piedfease response; IEA.
R OG. GG-0005952; Piedfease response; IEA.
R InterPro; IPR005639; endotoxin C.
R InterPro; IPR005639; endotoxin M.
R InterPro; IPR00555; endotoxin J.
Pfam; PP003944; endotoxin J.
Pfam; PP003945; endotoxin J.
R Pfam; PP003945; endotoxin J.
R Pfam; PR03945; endotoxin J.
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=29338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created}
Last sequence update)
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 97.9%;
Matches 1143; Conservative
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Shevelev A.B., Svarinsky M.A., Karasin A.I., Kogan Y.N.,
Chestukhina G., Stepanov V.M.;
"Primary structure of the cryX**-the novel Delta-endotoxin-related
gene from Bacillus thuringiensis ssp. galleriae.";
FRES Lett. 336:79-82 (1993).
HSSP; PO7130; 1DLC.
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NCBI_TaxID=1428;
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Last sequence update)
Last annotation update)
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      1118 TEQUWIDMSETEGUFNIESVELVLEEE 1144
                                                                                                                                                    PRT; 1144
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GO; GO:000592; P:defense response; IEA.
InterPro: IPR001178; Endotoxin.
InterPro: IPR005638; endotoxin.C.
InterPro: IPR005639; endotoxin.N.
Pfam; PP00555; endotoxin.I.
Pfam; PP00555; endotoxin.I.
Pfam; PP003945; endotoxin.C; 1.
Pfam; PP003945; endotoxin.N: 1.
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                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                           Bacillus thuringiensis
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STRAIN=HD-9;
Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
"Characterization of crylB gene and its flanking regions Bacillus thuringiensis subsp. entomocidus HD-9.";
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Bacteria: Firmicutes: Bacillales: Bacillaceae; Bacillus.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                         SYAGVLIMGIYLEPIHGVPTVRPNPTNPQNISDR-GTANYSQPYBSPGLQLKDSET--EL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPE--NEPLSRGYSHRISHITSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVYSDXIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECLSDELYPNEKRMLWDAVKEAKRLVQARNILLQDTGFNRIN-----
                                                                                                                                                                                                                                                                                            KTF1SSSTVQTG1G1VGQVLGALGVPPAGQ1ASFYSF1VGQLWPSSTVSVWEMIMKQVED
                                                                                                                                                                                                                1 MSPNNONEYEILDASSSTSVSDNSVRYPLANDOTTTLONMNYKDYLRMSEGENPELFGNP
                                                                                                                                                                                                                                      Gaps
                                                                                                                                     Query Match
42.1%; Score 2545.5; DB 2; Length 1228;
Best Local Similarity 43.8%; Pred. No. 1.6e-136;
Matches 558; Conservative 183; Mismatches 381; Indels 151;
InterPro; IPR008539; endotoxin N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PP00855; endotoxin; 1.
Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endotoxin_N; 1.
SEQUENCE 1228 AA; 139621 MM; 3DA2A4DBF59C95C3
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162 NAMPLFAIRNQEVPLIAMVYAQAANIAHILILRDASLFGSEFGLTSQEIQRYYERQVERTRD 221 241 YSDYCVKMYNTGLDKIKGTNAASWLKYHQFRREMTLLVLDLVALFPNYDTRTYPIETTAQ 300 241 YSDYCVKMYNTGLDKIKGTNAASWLKYHQFRREMTLLVLDLVALFPNYDTRTYPIETTAQ 300 222 YSDYCVEMYNTGLAKSTNAASWVRYNQFRRDLTLGVLDVALFPSYDTRTYPINTSAQ 281	301 LTREVYTDPIVENRETSGGFCRRWSLASDISFSEVESAVIRSPHLFDILSEIBFYTTRAG 360 	361 LPLANTEYLEYWYGHSIKYKNTNASSALBRNYGTITSNKIKYYDLANKDIFQVR 414 	415 SLGADLANYXAQVYGVPASFTLLDKNTGSGSVGGFTYSKPHTTMQVCTGNYNTIDBI 472	473 PPENEPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVPAWTHRSADVTNTVYSDKIT 530	531 QIPVVKAHTLVSGTTVIKGPGFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYAST 590 [:	591 TMLRLFVTISGTRIYSINVNKTWAKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFA 650 	651 SGGBYYVDKFELIPVNATFRAEEDLDVAKKAVNGLFTSKKD-ALQTSVTDYQVNQAANLV 709 	710 BCLSDELYPNEKRMLWDAVKEARRLVQARNLLQDTGFNRIN750 : 681 ACLSDEPCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHE 740	751 -GENGWTGSTGIEVABGDVLFKDRSLRLTSARBIDTETYPTYLYQQIDESLLKPYTRYKL 809 	810 KGFIGSSQDLEIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCŠEQOYVDANL 865 	866 ALENNGENG-NMSSDSHAFSFHIDTGEIDLNENTGIWVVFKI PTTNGYATLGNLELVEEG 924 ::: :	925 PLSGETLERAQQQQQQQQQQQQDXMARKGASEKAYYAAKQALDRLFADYQDQKLNSGVEMSDM 984 	985 LAAQNLVQSIPYVYNDALPEIPGMNYTSPTELTNRLQQAWNLYDLRNAIPNGLSD 1044 	1045 WNATSDVAVQQLSDTSVLVIPNWNSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVIIRDG 1104 	1105 ANQTETLIF1113 :	1114NICDDDTGVLSADQTSYITKTVEFTPSTEQVMIDMSETEGV 1154 : : :	1155 FWIESVELVLEER 1167 :: : 1216 FIVDSVELLLARB 1228
a & a	ራ 4	& 4	රි සි	දු දු	රි සි	පු ද	ò 8	중 <u>원</u>	ò 8	ර සි	8	<i>8</i> €	& 8	& a	& 8	& 8	& 4
Db 856 DLDCSCRDGEKCAHHSHHFSLDIDVGCTDLHENLGVWVVFKIKTQBGHARLGNLEFIEEK 915 Qy 925 PLSGETLERAQQQEQQWQDKWARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDM 984	OY 985 LAAONLVQSIPYVYNDALPEIRGANYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSD 1044	OY 1045 WNATSDVNVQQLSDTSVLVIPNWNSQVSQOFTVQPNYRYVLRVTARKBGVGDGYVIIRDG 1104	OY 1105 ANQTETLTP 1113 :	NICDDDTGVLSADQTSYITKTVEFTPSTEQVWIDMSETBGV : : : : :		RESULT 4 093NM5	ID Q93NM5 PRELIMINARY, PRT; 1228 AA. AC Q93NM5, DT 01-DBC-2001 (TrEMBLrel. 19, Created) DT 01-DBC-2001 (TrEMBLrel. 19, Last sequence update)				DR GO; GO:0006952; P:defense response; IEA. DR InterPro; IPR001178; Endotoxin. C. DR InterPro; IPR005638; endotoxin. C. DR InterPro; IPR005639; endotoxin. N.		SEQUENCE 1228 Anj 133000 An; SOUDSOLSTIESTS CACOT, Query Match 42.0%; Score 2539.5; DB 2; Length 1228; Best Local Similarity 43.8%; Pred. No. 35-2136; Autobio 657, Concounting 103, Winnethboo 920, Indole 151, Conc	MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKOYLRMSEGENPELFGNP 6	DD I MISORKARRELINAVSNBSA	121 LIDOKITDSVRKTALAGLOGGGDDDVQKSLKNWIENRNDTRARSVVVTQYIALELDFV	

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1033 NGDFNNGLSCWNVKGHVDVQQSHHRSDLVIPEWEAEVSQAVRVCPGRGYILRVTAYKBGY 1092
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                                                                                                                            YRARIRYASTINLRLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSD
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---PLAYTSVSVKSPLSQR
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"Cloning and expression of a delta endotoxin gene from a native Bacillus thuringiensis strain.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U94191; AAG16877.1; -
PIR; A29125; A29125.
HSSP; P02965; 1CIY.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Delta endotoxin.
Bacillus thuringiensis.
Bacteria; Pirmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TAXID=1428;
   IPVVKAHTLVSGTTVIKGPGFTGGNILKRTSSG-----
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1213 GETEGKFIVDSVELLLMEE
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167 TAIPLFRIRNEEVPLLAVYAQAANLHLLLLRDASLFGSEWGMASSDVNQYYQEQIRYTEE 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Island I.A., Isakov Y.B., Rymar' S.E., Yarovoi S.V.;
Cloning of a novel Bacillus thuringiensis crylBil gene for insecticidal crystal protein.", consistent of Aug. 2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX138457; AAM93496.1; -...
GO; GO:0005925; Pedefense response; IEA.
R GO; GO:0006952; Pedefense response; IEA.
R InterPro; IPR005639; endotoxin.C.
R InterPro; IPR005639; endotoxin.R.
R InterPro; IPR005639; endotoxin.R.
R InterPro; IPR005639; endotoxin.R.
R InterPro; IPR005639; endotoxin.C.
R Pfam; PP003944; endotoxin.C; 1.
R Pfam; PP03944; endotoxin.C; 1.
R Pfam; PP03945; endotoxin.R; 1.
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1231 AA; 139765 MW; C9F2848A9297EA00 CRC64;
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NCBI_TaxID=1428;
                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                1231 AA
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(TrEMBLrel. 22, I
(TrEMBLrel. 25, I
                                                                                                                                PRELIMINARY;
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01-0CT-2003 (
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GO; GO:0015070; F:toxin activity; IEA.
GO; GO:0016952; F:defense response; IEA.
InterPro; IPR001778; Endotoxin.
InterPro; IPR005638; endotoxin_C.
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TEGTFIVDSVELLLMEE 1155
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                                                                                                                                                                                                                                167;
                                                                                                                                                                                                2; Length 1155;
                                                                                                                                                                                             Query Match 34.0%; Score 2056.5; DB 2; Length Best Local Similarity 39.2%; Pred. No. 1.2e-108; Matches 477; Conservative 184; Mismatches 389; Indels
                                                                                                                                                             5D69E3B2F527749D CRC64;
GO; GO:0015070; F:toxin activity; IRA.
GO; GO:0006952; P:defense response; IRA.
InterPro; IPR001173; Endotoxin.
InterPro; IPR005639; endotoxin.
InterPro; IPR006539; endotoxin.N.
InterPro; IPR006579; Gal. bind_like.
Pfam: PP00555; endotoxin; 1.
Pfam: PP03944; endotoxin; C; 1.
Pfam: PP03945; endotoxin; C; 1.
SEQUENCE 1155 AA; 130557 WW; 5D695382P
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                                 NGLSDWINATSDVNV-QQLSDTSVLVI PNWNSQVSQQPTVQPNYRYVLRVTARKEGVGDGY
LVEEGPLSGETLERAQQQEQQWQDKWARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGV
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SPRCIES=B.t.buringlensis, STRAIN=T84A1;
SPRCIES=B.t.buringlensis, Hatanaka C., Funatsu G., Hayashi K.;
Nagamatsu Y., Itai Y., Hatanaka C., Funatsu G., Hayashi K.;
"A Toxic Fragment from the Entomocidal Crystal Protein of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sotto.";
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SPECIES-B.thuringiensis; STRAIN=T84A1;
Ogo M., Yamada S., Kobayashi Y., Shibata J., Nagamatsu Y.;
"Nuclectide Sequence of the Lepidoptera-toxic Protein Genethuringiensis subsp. dendrolimus T84A1.";
J. Fac. Appl. Biol. Sci. Hiroshima Univ. 29:95-107(1990).
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SEQUENCE FROM N.A.
Zhong C.X., Xiang Y.W.;
Zhong W.F., Cai P.Z., Yan W.Z., Zhang Z.X., Xiang Y.W.;
Zhong W.F., Cai P.Z., Yan W.Z., Zhang Z.X., Xiang Y.W.;
"A crylA gene cloned from Bacillus thuringiensis serovar i
Submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ABC026561; BAA77213.1; -.
EMBL; APS10713; AAM44305.1; -.
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Bacillus thuringiensis (subsp. sotto).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Nagamatsu Y.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Brie4A1 crystal protein (Crystal protein Crylh).
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| IPHGDFRNGLSDWNATSDVNV-QQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARK 1091
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                                           QKLINSGVEMSDMLAAQNLVQSI PYVYNDALPEI PGMNYTSFTELTNRLQQAWNLYDLRNA
                                                                                                                                                    EGVGDGYVIIRDGANQTETLTFN-----ICDDDTGV-----
                                                                                                                                                                                         -----LSADQTS------YITKTVEFTPSTEQ
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 ARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWBTNIVYKBAKBSVDALFVNSQY
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33.9%; Score 2048; DB 2; Length 1176;
Best Local Similarity 39.3%; Pred. No. 3.8e-108;
Matches 480; Conservative 174; Mismatches 414; Indels 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yao J., Zhang J., Song F., Chen Z., Li C., Huang D.;
"A novel crylaa gene from Bt atrain 1y30.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF344211; AAP80146.1; -
SEQUENCE 1176 AA; 133169 WW; 725C14EA9408869B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus
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Last sequence update)
Last annotation update)
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Bacillus thuringlensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae;
NCBI_TaxID=1428;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAGNAAPPVL--VSLTGLGIFRTLSSPLYRRIILGSGPNNQBLFVLDGTBFSFASLTTNL 397
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                                                                                                                        Gaps
                                                                                             33.9%; Score 2050; DB 2; Length 1180;
llarity 39.3%; Pred. No. 3e-108;
Conservative 173; Mismatches 414; Indels 156;
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PP00555; endotoxin; 1.
Pfam; PP03944; endotoxin C; 1.
Pfam; PP03945; endotoxin N; 1.
SEQUENCE 1180 AA; 133489 MW; 1199E4A6DIDCE62D CRC64;
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481; Conserv
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VLDLVALFPNYDTRTYPIETTAQLTREVYTDPIVFNRETS-CGPCRRWSLNSDISFSEVE 336
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                                        STRAIN=FU-2-7;
Kondo S., Tamura N., Kunitate A., Hattori M., Akashi A., Ohmori I.;
Kondo S., Tamura N., Kunitate A., Hattori M., Akashi A., Ohmori I.;
"Cloning and nucleotide sequencing of two insecticidal delta-endotoxin
genes from Bacillus thuringiensis var. kurstaki HD-1 DNA.";
Agric. Biol. Chem. 51:455-463(1987).
                                                                                                                                                                                                                                                                                                                                                                                                               | STAINTE-94289859; PubMed=7764972; | WREDLINE=94289859; PubMed=7764972; | Udayaeuriyan V., Nakamura A., Mori H., Masaki H., Uozumi T.; | Udayaeuriyan V., Nakamura A., Mori H., Masaki H., Uozumi T.; | Udayaeuriyan V., Nakamura A., Mori H., Masaki H., Uozumi T.; | Udayaeuriyan V., Nakamura A., Mori H., Morillus thuringienais strain FTU2-7 and analysis of chimaeric Cryld(a) proteins for toxicity."; | Biosci. Biotechnol. Biochem. 58:830-835(1994). | Biotechnol. Biochem. 58:830-835(1994). | PIR, JC2219; JC221
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33.8%; Score 2045; DB 2;
Best Local Similarity 39.3%; Pred. No. 5.7e-108;
Matches 479; Conservative 174; Mismatches 415;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=FU-2-7;
PROM N.A.
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(TremBirel. 01, Last sequence update)
(TremBirel. 25, Last annotation update)
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                        SGSFRIVGFTIPPNFSNGSSVFILSAHVFNSGNBVYIDRIEFVPABVTFBABYDLERAQK 621
                                                                                                                                                                                                  LLODIGPNRING--ENGWIGSTGIEVAEGDVLFKDRSLRLISARRIDIETYPTYLYQID 797
                                                                                                                                                                                                                                                     LLODPNFRGINROLDRGWRGSTD1T1QGGDDVFKENYVTLLGTFD---ECYPTYLYQKID 738
                                                                                                                                                                                                                                                                                                        ESLLKPYTRYKLKGFIGSSQDLEIKLIRHRANQIVKNVPDN----LLPDVLPVNSCGGID 853
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Bacillus thuringiensis (subsp. kurstaki).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ dat
EMBL, AF154676; AAD55382.1; -.
HSSP, P02965; ICTY.
GO, GO:0015070; F:toxin activity; IEA.
GO; GO:0015070; F:toxin activity; IEA.
InterPro: IPR001179; Endotoxin.
InterPro: IPR005539; endotoxin.
InterPro: IPR005539; endotoxin.
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Pfam; PP0555; endotoxin; 1.
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                                                                                                                                                                          AEMGPTPGBISTPYDRQVTRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLL
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                                                                                                                                    NRNDTRARSVVVTQYIALBLDFVAXIPSPAISGQEVPLLSVYAQAANLHLLLLRDASIFG
                                      Gaps
                  Length 1176;
                                      Indels
1176 AA; 133010 MW; FCEE069D0B81D8C4 CRC64;
                   33.7%; Score 2034; DB 2;
llarity 39.2%; Pred. No. 2.4e-107;
Conservative 173; Mismatches 417;
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                     S-IRSPHIMDILNSITIYT----DAHRGEY--YWSGHQIMASPVGFSGPEFTFPL---Y 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    742 KLKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETVNVPGT--GSLWPLSAPSPIGKCAHH-
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                                                                                                                                                                                                                                                    SGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLFVT16GTRIYSINVNKTMNKGDDLTFN
                                                                                                                                                                                                                                                                        ODTGFNRING--ENGWIGSTGIBVAEGDVLFKDRSLRLTSARBIDIETYPTYLYQQIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPPNFRGINRQLDRGWRGSTDITIQGGDDVFKRNYVILLGTFD---ECYPTYLYQKIDES
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                                                                                                                           447 VGGFTYSKPHTTMQVCTQNYNTIDBIPPENR--PLSRGYSHRLSHITSY--SPSKNASSP
                                                                                                                                                                                                          TPDLATIGTAFTFSNYSDSLTVGADSFASGGEVYVDKFELI PVNATFRAEBDLDVAKKAV
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                                                             GTITSNKIKYYDLANKDIPOVRSIGADLANYYAQVY--GVPYASPTLLDKNT----GSGS
                                                                                             GIMGNAAPQQRIVAQLGQGVYRTLSSTL---YRRPFNIGINNQQLSVLDGTEPAYGTSSN
                                                                                                                                                                                           503 ARYGNLPVFAWTHRSADVTNTVYSDKITQIPVVKAHTLVSGTTVIKGPGPTGGNILKRTS
                                                                                                                                              LPSAVYRKSGTV-----DSLDEIPPQNNWVPPRQGFSHRLSHVSMFRSGFSNSSVSI
AVIRSPHLFDILSEIBPYTTRAGLPLANNTEYLEYWVCHSIK----YKNTNASSALERNY
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Last sequence update)
Last annotation update)
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A Yu J., Tan L., Wu D., Pang Y.;

Tu J., Tan L., Wu D., Pang Y.;

"Molecular characterization of a silent gene encoding a 130-kilodalton of a region of a protein from Bacillue thuringiensis subsp. israelensis.";

Torystal protein from Bacillue thuringiensis subsp. israelensis.";

Torystal protein from Bacillue thuringiensis subsp. israelensis.";

E Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

R RML; A29125. A29125.

R GO; GO:0015070; F:toxin activity; IEA.

R GO; GO:0015070; F:toxin activity; IEA.

R GO; GO:0015070; F:toxin activity; IEA.

R InterPro; IPR00551; endotoxin.

R InterPro; IPR008979; Gal_bind_lke.

DR Pfam; PP00555; endotoxin.

DR Pfam; PP03945; endotoxin.

SQ SRQUENCR 1155 AA; 130747 MW; 7F0C98E01100C7698 CRC64;
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                          DTGVLSADQTS-----YITKTVEPTPSTEQVWID 1147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : : | : |: || :|| :|| DPTNPALREEMRIQFNDWNSALTTAIPLFAVQNYRVPLLSVYVQAVNLHLSVLRDVLVFG 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 VLDIVSLFPNYDSRTYPIRTVSQLTRRIYTNPVLENFD--GSF--RGSAQG-----IBG
   IPNGDFRNGLSDWNATSDVNV-QQLSDTSVLVIPNWNSQVSQQFTVQPNYRVVLRVTARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 NPEL-----PGNPET-FISSSTVQTG---IGI---VGQVLGALGVPFAGQIASFYSF
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33.6%; Score 2032.5; DB 2; Length
Best Local Similarity 38.9%; Pred. No. 2.9e-107;
Matches 473; Conservative 185; Mismatches 392; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Crystal protein CrylAbi6.
CRYLAB16.
Bacillus thuringiensis (subsp. israelensis).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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IGETEGTFIVDSVELLLMER 1176
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                                                                                 692 ALQTSVTDYQVNQAANLVECLSDELYPNEKRMLWDAVKRAKRLVQARNLLQDTGFNRIN-
                                                                                                                                                                                                                                                                                               PLSGETLERAQQQEQQWQDKMARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDM
508 INSPITQRYRLRFRYASSRDARITVAIGGQIRVDWTLBKTWBIGBSLTSRTFSYTNPSNP
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                                                     PTPSNYSDSLTVGADSPASGGEVYVDKPELIPVNATFEAEEDLDVAKKAVNGLFTSKKD-
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STRAIN-B-Pr-88;
Li C., Zhang J., Li G., Huang D.;
A Li C., Zhang J., Li G., Huang D.;
A crystal endotoxin from Bt strain.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
E EMBL, AF288683; AA013756.1;
A GO; GO:0015070; P:toxin activity; IEA.
A GO; GO:0006952; P:defense response; IEA.
A InterPro; IPR00178; Endotoxin.
A InterPro; IPR005639; endotoxin.
A InterPro; IPR008539; endotoxin.
A InterPro; IPR008549; endotoxin.
A InterPro; IPR008549; endotoxin.
A InterPro; IPR008559; endotoxin.
A InterPro; IPR008799; IRR05509; endotoxin.
A InterPro; IPR008799; IRR05509; endotoxin.
A INTERPO; IPR008799; IRR05509; Endotoxin.
A Pfam; PF03944; endoto
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Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Last annotation update)
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                                                                                                                                                                                                   Barboza-Corona J.B., Lopez-Meza J.B., Ibarra J.B.,
"Cloning and expression of the crylBa4 gene of Bacillus thuringiensis
and the comparative toxicity of its gene product.";
World J. Microbiol. Biotechnol. 14:437-441(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 33.4%; Score 2016.5; DB 2; Length 1171; al Similarity 38.3%; Pred. No. 2.4e-106; 464; Conservative 176; Mismatches 412; Indels 159;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-LEFT-147.

I Ibara J.E., Barboza-Corona J.E.;

Submitted (MR-1997) to the EMBL/GenBank/DDBJ databases.

Submitted (MR-1997) to the EMBL/GenBank/DDBJ databases.

EMBL: U494323; AAD04732.1; -.

PIR: A37829; A37829.

R GSP: GG:00165107; Fitoxin activity; IEA.

GO; GG:0006952; Pidefense response; IEA.

InterPro; IPR001178; Endotoxin. C.

InterPro; IPR005639; endotoxin. C.

InterPro; IPR005639; endotoxin. C.

R InterPro; IPR008979; Gal_bind_like.

Pfam; PP00555; endotoxin. 1.

Pfam; PP00344; endotoxin. N; 1.

Pfam; PP0344; endotoxin. N; 1.

SEQUENCE 1171 AA; 133310 MW; 333603A1A782523A CRC64;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
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                                                                                                                                [1] SEQUENCE FROM N.P
STRAIN=LBIT-147;
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960 YDARNVIKNGDFNNGLSCWNVKGHVDVEEQANHERSVLVVPEWEAEVSQEVRVCPGRGYIL 1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 WEMIMKQVEDLIDOKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIYPIETTAQLIREVYIDPIV-PNRETSGGFCRRWSLNSDISFSBVESAVIRSPHLPDIL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEIBFYTTRAGLPLANVIEYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKYYDLANKD 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 YDRQVTRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLLVLDLVALFPNYDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYIALBLDFVAKIPSFAISGQBVPLLSVYAQAANLHLLLLRDASIFGABWGFTPGBISTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1189;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN=A2-F;

STRAIN=A2-F;

Tu J., Pang Y., Li J.;

"Cloning and sequence analysis of the crylCa6 gene from Baci thuringiensis, strain A2-F.";

Luningiensis, strain A2-F.";

Luningiensis, strain A2-F.";

E WHM: A215647; AA27324-1;

R GO; GO:0010510; P:toxin activity; IEA.

R GO; GO:0006952; P:defense response; IEA.

R InterPro; IPR001178; Endotoxin.

R InterPro; IPR005639; endotoxin. N.

R Pfam; PF013944; endotoxin. C; 1.

R Pfam; PF013945; endotoxin. N.

R Pfam; PF013945; endotoxin. N.
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Bacillus thuringiensis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1428;
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                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1997; DB 2;
Pred. No. 3.2e-105;
                                                                                                                                  1138 TPSTEQUWIDMSETEGVFNIBSVELVLEEE 1167
                                                                                                                                                 RVTARKEGVGDGYVI IRDGANOTETLTFN----
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38.3%; Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   -:---TSLVEGVGFIQPNNGEQLYRVRGTLDSLDQLPLEGESSLTEXSHRLCHVRPAQ 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 SFYSFIVGQLWPSSTVSVWEMIMKQVEDLIDQKITDSVRKTALAGLQGLGDGLDVYQKSL 152
                                                                                                                                                               280 -----VLREPHIADFLNRLIIYT------GEYRGIRHWAGHEVESSRIGAMINIRF 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLRNA-EPLDYARVPMFSWTHRSATPTNTIDPDVITQIPLVKAFNLHSGATVVRGFGFTG 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYQQIDESLLKPYTRYKLKGPIGSSQDLRIKLIRHRANQIVKNVPDN----LLPDVLPVN 847
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                                                                                                                                                                                                                                                                        EMTLLVLDLVALPPNYDTRTYPIETTAQLTREVYTDPIVFNRETSGGFCRRWSLNSDISP
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                                                                    Gaps
                                        Query Match
33.1%; Score 2003; DB 2; Length 1169;
Best Local Similarity 39.3%; Pred. No. 1.4e-105;
Matches 460; Conservative 173; Mismatches 389; Indels 148;
  Pfam; PF03945; endotoxin_N; 1.
SEQUENCE 1169 AA; 132990 MW; 07C9D6D180F3DB6D CRC64;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBL_TaxID=1428;

SEQUENCE FROM N.A

INFORMATION." STRAIN=BTS00349A;

8

Lambert

Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases [2]

SEQUENCE PROM N.A. STRAIN=B-Pr-88;

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                                                                                                                                                                                                                                                                                                                                                                                      NNLTIFTDWFSVGRN----FYWGGHRVISSLIGGGNITSPIYGREANQEPPRSFTFNGP 359
               IFQVRSLGADLANYYAQVYGVPYASFTLLDKNTGSGSVGGFTYSKPHTTWQVCTQNYNTI 469
                              360 VP--RILSNPTLRILLQQPWPAPPPINLRGVEGVEFSTPTNSFTYRGRGTV-----DSL 409
                                              DEIPPENE--PLSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVYSD 527
                                                        |:|||: | |||||| | | | : :|
TELPPEDNSVPPREGYSHRLCHAT---FVQRSGTPFLTTGV-VFSWTHRSATLTWTIDPE 465
                                                                                                                  640
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                                                                                                                                                                                                                                                                                                                       KITQIPVVKAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRY
                                                                                                              ASTTNLALPVT----ISGTRIYSINVNKTMNKGDDLIFNTFDLATIGTAFTPSNYSD
                                                                                                                        ENGWTGSTGIEVARGDVLPKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYRLKG
                                                                                                                                                                                                                      ENNGENG-NWSSDSHAFSFHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVERGPL
                                                                                                                                             SLTV-----GADSPASGGEVYVDKFELIPVNATFEAEEDLDVAKKAVNGLFTSKKD-AL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : :| || | : :| || 356 YRTLSDPVF-VRG-GPGNPHYVLGLRGVAP------QQTGTN------HTRTFRN 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                59 NPETFISSSTVQTG-----IGIVGQVLGALGVPPAGQIASFYSFIVGQLMPSSTVSVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 YIALELDEVAKIPSPAISGOEVPLLSVYAQAANLHLLLLLRDASIFGAEWGFTPGEISTFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRQVTRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLLVLDLVALFPNYDTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 IBFYTTRAGLPLNNTBYLEYWYGHSIKYNNTNASSALERNYGTIT-----SNKIKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPIRITAQLTREVYTDPIVFNRETSGGFCRRWSLNSDISFSBVBSAVIRSPHLFDILSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TONYNTIDEIPPENEPLS--RGYSHRLSHITSYSFSKNASSPARYGNLPVPANTHRSADV
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                                                                                                                                                                                                                                                                                                                                                      Query Match 32.9%; Score 1989.5; DB 2; Length 1174; Best Local Similarity 38.0%; Pred. No. 8.4e-105; Matches 458; Conservative 191; Mismatches 413; Indels 143;
A Li C., Zhang J., Huang D., Li G.;

"A crystal endotoxin from Bacillus thuringiensis strain B-Pr
Submitted (JAN-2001) to the EWEL/GenBank/DDBJ databases.
L Submitted (JAN-2001) to the EWEL/GenBank/DDBJ databases.
EWEND: 222512; CAA80235-1; -.
EWEND: 322649; S32649.
R HSSP; P02965; LCIY.
R GO; GO:0005695; LCIX.
R GO; GO:0005695; P:defense response; IEA.
R GO; GO:0006952; P:defense response; IEA.
R InterPro; IPR001178; Endotoxin.
R InterPro; IPR005639; endotoxin.
R InterPro; IPR005639; endotoxin.
R InterPro; IPR005639; endotoxin.
R InterPro; IPR005639; endotoxin.
R Pfam; PP003944; endotoxin. C; 1.
R Pfam; PP003944; endotoxin. C; 1.
R Pfam; PP03945; endotoxin. Z; 1.
R Pfam; PP03945; endotoxin. N; 1.
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045749; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Crystal protein (Crystal delta-endotoxin). CRYIFB.

PRELIMINARY;

045749

045749 1D 049 AC 044 DT 011 DT 010 DE CT 08

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993 SIPYVYNDALPEIPGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVN 1052
                                                                                                                                                                                                                                         1112 TF---- 1113
                                                                                                                                                                                                                                                        1050 KPSNCVEEGYPNNTVTCNEYTMNQGVGECTDACNVRNRGYEDAYGHNPSTPVHYTTPYEE 1109
                                                                                                                                                          STGIEVARGDVLPKDRSLRLTSARRIDTETYPTYLYQQIDESLLKPYTRYKLKGFIGSSQ 817
                                                                  DLEIYLIRYNSKHEIVAVVPGTGSLWPLSVENQIGPCGEPURCA--PHLEWNPDLHCSCRD 809
                                                                                                                    GNMS-SDSHARSFHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVEEGPLSGETLE 932
                                                                                                                            933 RAQQQEQQWQDKMARKRGASEKAYYAAKQAIDRLFADYQDQKINSGVEMSDMLAAQNIVQ 992
                                                                                                                                                                                       930 RIREAYLPELSVIPGVAAAIFEELEGRIFTAYSLYDARNVIKOGNFNNGLLCWNVKGHVD 989
                                                                                       DLEIKLIRHRANQIVKNVP--DNLLPDVL--PVNSCGGIDRCSEQQYVDANLALENNGEN 873
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1170 LLMEE 1174
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June 21, 2004, 13:35:05; Search time 28 Seconds (without alignments) 4009:125 Million cell updates/sec US-10-089-678-1 6044 1 MSPNNQNEYELLDASSSTSV......MSETEGVFNIESVELVLEEE 1167

Title: Perfect score: Sequence: Scoring table:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match O% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		parasporat crystal	parasporal crystal	٦	parasporal crystal	_	parasporal crystal	_	_	parasporal crystal	parasporal crystal	_	parasporal crystal	parasporal crystal	parasporal crystal	parasporal crystal	_	parasporal crystal	parasporal crystal	parasporal crystal	_	_	parasporal crystal	parasporal crystal	-	parasporal crystal	parasporal crystal	parasporal crystal
ID	140589	549647	S00873	A48944	S19306	A42459	S32645	A26513	JD0002	S02134	JT0241	JC2219	A41052	A29125	802215	A22617	139838	I40572	A37829	S32649	S00944	S32647	S11446	USBSXH	A29838	A49785	A48970	S32689
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Length	1160	115/	1228	1138	1156	1174	1166	1155	1155	1155	1176	1176	1181	1156	1176	1176	1155	1171	1171	1174	1189	1160	1165	1178	1156	1177	1176	1172
누드	61.8	77.7		40.7	36.3	35.6	34.6	34.2	34.1	34.0	33.9	33.8	33.8	33.8	33.7	33.7	33.6	33.5	33.3	32.9	32.8	32.3	32.2	32.1	32.0	31.9	31.8	31.7
Score	3733.5	3123		2458.5	2191	2154.5	2093.5	. 2064.5	2061.5	2052.5	2048	2045	2044.5	2043	2038	2037	2030.5	2024.5	2010.5	1989.5	1984	1953.5	1944	1939	1932	1930.5	1923.5	1917
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parasporal crystal parasporal crystal parasporal crystal cryv465 protein - insecticidal prote parasporal crystal insecticidal prote parasporal crystal	hypothetical prote
USBSBI 139870 AA6858 AA6858 139815 525383 139814 139811 139811 139811 139838 AZ7323 AZ7323 UAC7140	B42459
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1136 1180 1180 719 719 719 823 652 652 652 653 653	380
2000 2000 2000 2000 2000 2000 2000 200	17.6
1868.5 1772.5 1772.5 1732.5 1733.5 1683.5 1272.5 1272.5 1132.5 1132.5 1066.5	1001
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ALIGNMENTS

RESULT 1	
I40589 paragnoral	140589 paragnoral crystal protein cry8Cal - Bacillus thuringiensis
N, Alternate	Management angles: parasporal crystal protein crylli
C; Date: 12.	Cipperion: Date: 12-Aug-1906 #sequence_revision 12-Aug-1996 #text_change 01-Dec-2000
R,Sato, R., Takeuch:	ii 140369 Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; Asam
Curr. Micre	Curr. Microbiol. 28, 15-19, 1994
A; Reference	A;IITIE: CIONING, NECETOLOGOUB EXPRESSION, AND IOCALIZALION OL A NOVEL CLYSCAL PIOCELN: A;Reference number: 140589; MUID:94100786; PMID:7764305
A, Accession	1: I40589
A;Status: preliminar A;Molecule type: DNA	A;Status: preliminary; translated trom GB/EMBL/DDBJ A;Molecule type: DNA
A; Residues: A; Cross-rei	A;Residues: 1-1160 <res> A;Cross-references: EMBL:U04366; NID:g532523; PIDN:AAA21119.1; PID:g532524</res>
C, Superfam C, Keywords	C,Superfamily: parasporal crystal protein C,Keywords: delta-endotoxin
Query Mat	ch 61.8%; Score 3733.5; DB 2; Length 1160;
Best Loca Matches	Best Local Similarity 64.2%; Pred. No. 1.6e-208; Matches 767; Conservative 109; Mismatches 257; Indels 61; Gaps 21;
ò	1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLANSEGENPELFGNP 60
අු	
ò	61 BTPISS-STVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQL#PSSTVSVWEMIMKQVB 119
QQ	61 GTPISAQDAVGTGIDIVSTIISGLGIPVLGEVPSILGSLIGILAPSINENVAQIFMARVE 120
\$	120 DLIDOKITDSVRKTALAGLOGIGDGIDVYQKSLKAWLENRNDTRARSVVVTQYIALELDF 179
Dp 1	121 BLIDQKILDSVRSRALADLANSRIAVBYYQNALEDWRKNPHSTRSAALVKERFGNAEAIL 180
&	80 VAKIPSPAISGOBVPLLSVYAQAANLHILLIRDASIPGAEMGFTPGEISTFYDRQVTRTA 239
q	181 RTNMGSFSQTNYETPLLETYAQAASLHLLVMRDVQIYGKEWGYPQNDIDLFYKEQVSYTA 240
8	240 QYSDYCVKWYNTGLDKIKGTNAASWIKKHQFRREWILLVLDLVALFPNYDTRIYPIETTA 299
e e	: : : : : : : :
8	300 QLTREVTIDPIVFNRETSGGPCRRWSLNSDISFSEVBSAVIRSPHLPDIL 349
ą	301 BLTREIFTDPVGSYVTGQSSTLISWYDMIPAALPSFSTLEN-LLEKKPDFFTLL 352

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ΩĐ	:: : :	Best Lo	Best Local Similarity 52.3%; Pred. No. 4.4e-173; Matches 619; Conservative 195; Mismatches 327; Indels 42; Gaps 14;
8	IDEIPPENBPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVY	ò	MSPNNQNEYELLDASSSTSVSDNSVRYPLANDQTTTLQNANYKOYLRMSRGENPELFGNP
셤	455 IDSGEELTYENYQSYSHRVSYITSFEIKSTGGTVLGVVPIRGWTHSSASRNNPIY 509	ସ୍ପ	1 MORINIONEYEIIDAPHCGCPSDDDVRYPLASDPNAALQNWNYKDYLQMTDEDYTDSYINP 60
ት ብ	526 SDKITQIPVVKAHTLVSGTTVIKGPG-FTGGNILKRTSSGPLAYTSVSVKSPLSQRY 581 : : :	<i>∂</i> ; 8	61 ETFISS-STVQTGIGIVGQVLQALGVPAGQIASFYSFIVGQLMPSSTVSVWEMIMKQVE 119
È	582 RARIKYASTINLELEVIISGTRIYSINVNKTMAKGDDLFENTFDLATICTA-F 633	ò	/YOKSLKNWLE
q		යි	LONWLADRNDTRNLSVVRAQFIAI
ò	634 TFSNYSDSLTVGADSFASGGBVYYDKFELIPVNATFBABEDLDVAKKANNGLFTSKKDAL 693	ð	180 VAKIPSFAISGQEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTFGEISTFYDRQVIRTA 239
οgα	627 GISGSSRIFDISITKEAGAANLYIDRIEFIFVNTLFFRAEBDLDVAKKAVNGLFTNEKDAL 686	qa	181 VNAIPLFAVNGOQVPILSVYAQAVNIHLILLKDASLFGEGWGFTQGEISTYYDRQLELTA 240
ò	694 QTSVTDYQVNQAANLVECLSDELYPNEKRMLWDAVKBAKRLVQARNLLQDTGFNRINGEN 753	ò	240 QYSDYCVKWYNTGLDKLKGTNAASWLKYHOPRREMTLLVLDLVALFPNYDTRTYPIETTA 299
d d	697 QTSVTDYQVNQAANLIECLSBELYPNEKRMLWDAVKBAKRLVQARNILLQDTGFNRINGEN 746	qq	241 KYTNYCETWYNTGLDRIRGTNTESWIRYHQFRREMTLVVLDVVALFPYYDVRLYPTGSNP 300
à	754 GWTGSTGIEVARGDVLFKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFI 813	ò	300 QLTREVYTDPIVFNRETSGGFCRRWSLANSDISFSEVESAVIRSPHLFDILSEIBFYTTRA 359
ΩÞ	747 GWTGSTGIEVVEGDVLFKDRSLRISAREIDTETYPTYLYQQIDESLLKPYTKYKLKGFI 806	qq	301 QLTREVYTDPIVFNPPANVGLCRRWGTNPYNTFSELENAFIRPPHLFDRLNSLTISSNR- 359
ò	814 GSSQDLEIKLIRHRANQIVKNVPDNILPDVLPVNSCGGIDRCSEQQYVDANLALENNGEN 873	ò	360 GLPLNYTEYLEYWVGHSIKYRNTNASSALERNYGTITSNKIKYYDLANKDIPQVRSL 416
g	807 GSSQDLEIKLIRHRANQIVKNVPDNILLPDVRPVNSCGGVDRCSEQQYVDANLALENNGEN 866	qa .	360 - FPV-SSNFMDYMSGHTLRRSYLNDSAVQEDSYGLITTRATINPGVDGTNRIEST 413
È	874 GNMSSDSHAPSFHIDTGEIDLMENTGIWVVFKIPTTNGYATLGNLELVERGPLSGETLER 933	õ	417 GADLANYYAQVYGVPYASFILLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP 474
qq	867 GNMSSDSHAPSFHIDTGEIDLNENTGIWIVPKIPTTNGNATLGNLBFVEEGPLSGETLEW 926	qq	414 AVDERSALIGIYGVRARASFVPGGLENGTTSPANGGCRDLYDTNDELPP 461
ઠે	934 AQQQEQQWQDKMARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQS 993	ò	475 ENEPLSRGYS-HRLSHITSYSPSRN-ASSPARYGNLPVFAWTHRSADVTNTVYSDKITQI 532
qq	927 AQQQEQQWQDKMARKRAASBKTYYAAKQAIDRLFADYQDQKLNSGVEMSDLLAAQNLVQS 986	qq	PPSPQTNQAGSIANAGSVP
È	994 IPYVYNDALPEIPGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNV 1053	ð	533 PVVKAHTLVSGTTVIKGPGFTGGNILKRTSSGPLAYTSVSVKSPLSGRYRARIRYASTTN 592
QQ	987 IPYVYNDALPEIPGMNYTSFTELTNRLQQAMNLYDLQNAIPNGDFRNGLSNWINATSDVNV 1046	qq	GGGILRRTINGTFGTLRVIVNSPLTQQYRL
è	1054 QQLSDTSVLVIPNWNSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTF 1113	ò	593 LALFVIISGTRIYSINVNKIMNKGDDLTFNIFDLATIGTAPTFSNYSDSLTVGA 646
Op QD	1047 QQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTF 1106	qq	Ö.
à	1114 NICDDDTGVLSADQTSYITKTVEFTPSTEQVWIDMSETEGVFNIESVELVLEEB 1167	ò	647 DSFASGGEVYVDKFELIPVNATFEAEBDLDVAKKAVNGLFTSKKDALQTSYTDYQVNQAA 706
qg	1107 NICDDDTGVLSTDQTSYITKTVEFTPSTEQVWIDMSFTEGVFNIESVELVLEER 1160	qq	RIEIVPVNPAREABEDI
1000		ò	707 NLVECLSDBLYPNEKRMIMDAVKEARRLVQARNILQDIGFNRINGBNGWIGSTGIEVA 764
S49247	2. 2	셤	699 NLVSCLSDEQYGHDKKMILLEAVRAAKRLSREKNILQDPDFNTINSTERNGWRASNGVTIS 758

parasporal crystal protein cry9Cal [validated] - Bacillus thuringiensis
Naletrate names: parasporal crystal protein cryIH
Naletrate names: parasporal crystal protein cryIH
C;Species: Bacillus thuringiensis
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Accession: A59350; A9247
R;Lambert, B.; Buysse, L.; Decock, C.; Jansens, S.; Piens, C.; Saey, B.; Seurinck, J.; Appl. Brviron. Microbiol. 62, 80-86, 1996
A;Title. A Bacillus thuringiensis insecticidal crystal protein with a high activity again A;Reference number: A59350; MUD:96141404; PMID:8572715
A;Accession: A59350
A;Molecule type: DNA
A;Residues: 1-1157 cLAM>
A;Cross-references: EMBL:237527; NID:9547554; PIDN:CAA85764.1; PID:9547556
A;Experimental source: serovar tolworthi
C;Comment: This parasporal crystal protein, active against corn borer and other insects, C;Superfamily: parasporal crystal protein
C;Superfamily: parasporal crystal protein

1004

FHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVBEGPLSGETLERAQQQEQQMQDK 944

SYINTGDLMASVOQGIWVVLKVRTTDGYATLGNLELVEVGPLSGESLEREQRDNAKWNAE

HHHKVHLVKNVPDNLVSDTYSDGSCSGINRCDBQPQWQLDAEHHPWDCCRAAQTHBFS

815

885 875

825

759

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RHRANGIVRAVPDNILLPDVILPVNSCGGIDRCSBQQYVDANLALENNGBNGNMSSDSHAFS

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292

824

884 874 | IPGMAYTSFTELTNRLQQAMNLYDLRNA| PNGDPRNGLSDWANTSDVNVQQLSDTSVLVI | 1064

MARKRGASEKAYYAAKQAIDRLFADYQDQKINSGVEMSDMIAAQNIVQSIPYVYNDALPE

945

935

1005

51.7%; Score 3123; DB 1; Length 1157;

Match Query

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parasporal crystal protein cryBal - Bacillus thuringiensis subsp. thuringiensis
NiAlternate names: parasporal crystal protein cryAA
NiAlternate names: parasporal crystal protein cryAA
C;Species: Bacillus thuringiensis subsp. thuringiensis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Dec-2000
C;Accession: S00873
R;Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus A;Reference number: S00873; MUID:88203216; PMID:3362680
A;Accession: S00873
A;Molecule type: DNA
A;Residues: 1-1228 <br/>A;Accession: S00873; MUID:940264; PIDN:CAA29898.1; PID:9580949
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                                                                        RNILLQDTGFNRING--RNGWTGSTGIBVARGDVLFKDRSLRLTSARBIDTETYPTVLYQQ
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                          DLTFWIFDLATIGTAFTFSNYSDSLTVGADSFASGGEVYVDKFELIPVNATFFABEDLDV
                                                                                                                                                                        AKKAVNGLFTSKEDALQTSVTDYQVNQAANLVECLSDELYPNBKRMLWDAVKBAKRLVQA
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43.8%; Pred. No. 1.3e-139;
ive 183; Mismatches 381;
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Keywords: delta-endotoxin
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A;Start codon: TTG
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N;Alternate names: delta-endotoxin-related protein; parasporal crystal protein cryX
C;Species: Bacillus thuringiensis
C;Date: 07-0ct-1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
C;Accession: S39536
R;Shevelev, A.B.; Svarinsky, M.A.; Karasin, A.I.; Kogan, Y.N.; Chestukhina, G.G.; Stepan PEBS Lett. 336, 79-82, 1993
A;Title: Primary structure of the cryX, the novel delta-endotoxin-related gene from Baci
                                                                                                   SHWDAQVSQQLRVNPNCKYVLRVTARKVGGGGGYVTIRDGAHQGTLTFNACDYDVNGTY 1114
995 IPGINYBIYTELSDRLQQASYLYTSRNAVQNGDFNSGLDSWNTTMDASVQQDGNMHFLVL 1054
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                                                                        PNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVI I RDGANQTBTLTFNI CDDDTGVLS
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RRNYGSTTS-IVNYFSFNDRDVYQINTRSHTGLGFQN--APLFGITRAQF
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A,Status: preliminary
A,Folecule type: DNA
A,Residues: 1-1154 <SHE>
A,Cross-references: RMEL:X75019
C,Superfamily: parasporal crystal pr
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Matches 562
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qq	43 DPFVSASTVQTGINIAGRILGVLGVPPAGQLASFYSFLVGELWPRGR-DQWBIFLEHVEQ 101	
Ś	121 LIDOKITDSVRKTALAGLOGLGDGLDVYOKSLKNWILENRNDTRARSVVVTOYIALELDFV 180	Oy 1114
; A		Db 1156 NYKP
ò		Oy 1155 PNIES
ପୁଘ	:	Db 1216 FIVDS
è	241 YSDYCVKWYNTGLDKLKGTNAASWLKYHOPRREWTLLVLDLVALPPNYDTRTYPIBITTAQ 300	RESULT 5
QΩ		parasporal crystal
ò	301 LTREVYIDPIVFNRETSGGFCRRWSLANSDISFSEVESAVIRSPHLPDILSBIBFYITRAG 360	N;Alternate names: C;Species: Bacillu C;Date: 19-Dec-199
qq	282 LTREVYTDAIGATGVNMASMNWYNNNAPSFSAIRAAAIRSPHLLDFLEQLTIFSAS 337	C;Accession: A4894 R;Lambert, B.; Hof
ò	361 LPLANTEYLEYWVGHSIKYKNTNBSSALERNYGTITSNKIKYYDLANKDIFQVR 414 	Appl. Environ. Mic A;Title: Novel Bac
đ	338 SRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRPASRDVYRTE 391	A;Reference number A;Contents: BTS137
È	SLGADLANYYAQVYGVPYASPTLLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBI	A; Accession: A4894 A; Status: prelimir
đ	392 SYAGVILMGIYLEPIHGVPTVRFNFTNPQNISDR-GTANYSQPYESPGLQLKDSETEL 448	A;Molecule type: I A;Residues: 1-1138
È	473 PPBNEPLSRGYSHRISHITSYSFSKNASSPARYGNIPVPAWTHRSADVINITVYSDKIT 530 44.9 DEFTOR DEPTOR SHIGHTITINGS - NAMEDVSGFTHSADPINITYSDRPT 500	A;Cross-references: A;Note: sequence ex
3		C; Keywords: delta-
දි දි	531 QIPVVKAHTLVSGTTVVKGPCFTGGNILKRTSSGPLAYTSVKVSBLSGYRALIKTAST 590	Query Match Best Local Simil
ઠ	591 TNIRLFVTISGTRIYSINVNKTMAKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFA 650	Matches 514; Co
7 A		ਜ '
ò	651 SGGEVYVDKFELIPVNATFRAREDLDVAKKAVNGLFTSKKD-ALQTSVTDYQVNQAANLV 709	H
· 원		
Š	710 BCLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRIN750	ů,
qa		
ò	751 -GENGWTGSTGIEVABGDVLFXDRSLRLTSAREIDTBTYPTYLYQQIDESLLKPYTRYKL 809	110
e da		
ò	810 KGFIGSSODLEIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQOYVDANL 865	0/1
qq		241 ISDI - - -
È	866 ALENNCENG-NMSSDSHAPSPHIDTGEIDLINENTGIWVVFKIPTTNGYATLGNLELVEBG 924	
д	856 DLDCSCRDGEKCAHHSHHFSLDIDVGCTDLHENLGV#VVFKIKTQBGHARLGNLEFIEEK 915	 Db
ð :	PLSGETLERAQQQEQQMQDIQMARKRGASEKAYYAAKQAIDRLPADYQDQKLNSGVEMSDM	Qy 359 AGLPI
වූ .	PLLGBALSRVKRABKKMRDKREKLOLBTKRVYTBAKEAVDALFVDSQYDRLQADTNIGMI	Db 339 YKAF
è 1	985 IAAQNIVQSIPYYINDALPEIPGANYTSFTELTNRIQQAMNLYDDANALPNGDRENGLSD 1044	Oy 416 LGADI
g 8	HAMMAN VIRLIKEALLEDELFVILECVINABLF BELEGGIJI I ALD ULI DAKIN VANGEFRINGLI. C. salimoniativoj openciji sti damanovijos odenijanja spravija tedo	Db 399 APSW
÷ a		
ò	1105 ANQTETLTP 1113	447
. a ,	: 1096 ENNTDELKFKNREEEEVYPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASV 1155	Oy 534 WKAI

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iofte, H.; Annys, K.; Jansens, S.; Soetaert, P.; Peferoen, M. tlcrobiol. 58, 2536-2542, 1992 acillus thuringiensis insecticidal crystal protein with a silent activi 37J
120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLNNTE-YLEYWYGHSIKYKNTNASSALERNYGTITSNKIK--YYDLANKDIFQVRS 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JLANYYAQVYGVPYASFILLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDEIPPE 475
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parasporal crystal protein cryIIIC
s thuringiensis
#sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISSSTVQTGIGIVGQVLGALGVPPAGQIASFYSPIVGQLWPSSTVSVWEMIMKQVED
                                                                                                                                                                                                                                                                                                                                                                                                s: GB:M64478; NID:g142760; PIDN:AAA22351.1; PID:g142761
extracted from NCBI backbone (NCBIN:112092, NCBIP:112093)
rasporal crystal protein
endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.7%; Score 2458.5; DB 2; Length 1138;
larity 43.5%; Pred. No. 1.6e-134;
Conservative 208; Mismatches 400; Indels 59;
                                                                                 SSVELVLEER 1167
                                                                                                                                                                                                                                                                                                                                                                      DNA; protein
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SSSTVQTGIGIVGQ------VLGALGVP-PAGQIASPYSFIVGQLWPSSTVSVWE 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDLENA-IPNPRPSWFLNNMIISTGSLTLPVSPSTDRARVWYGSRDRISPANSQFITELI 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTGFNRING--ENGWIGSTGIBVARGDVLFKDRSLRLTSARRIDTBTYPTYLYQQIDBSL
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                                                                                                                                                                5 NONEYBILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSBGBNPBLFGNPETFI
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(NCBIN:92865, NCBIP:92867)
                                                                                                                               98;
                                                                                                                               Indels
                                                                                                Length
                                                                                                                                                                                               2 NONKHGIIGASNCGCASDDVAKYPLANNPYSSALNLN------
                                                                                               Query Match 36.3%; Score 2191; DB 2; Best Local Similarity 41.5%; Pred. No. 5.7e-119; Matches 501; Conservative 195; Mismatches 414;
 extracted from NCBI backbone
                               A;Gene: cryIG
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
   sequence
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C;Genetics:
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S19306
S19306
Sparasporal crystal protein cry9hal - Bacillus thuringiensis
NyAlternate names: delta-endotoxin; insecticidal crystal protein; parasporal crystal prof. Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: 04-Dec-1992 #sequence revision 04-Dec-1992 #text_change 01-Dec-2000
C;Accession: S19306; S23588; A44847; S14602; S14837
R;Smulevitch, S.V.; Osterman, A.L.; Shevelev, A.B.; Kaluger, S.V.; Karasin, A.I.; Kadyrd FEBS Lett. 293, 25-28, 1991
A;Title: Nucleotide sequence of a novel delta-endotoxin gene cry1g of Bacillus thuringie A;Accession: S19306; MUID:92070568; PMID:1660003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Wolecule type: protein
A;Residues: 24-34 <SMU1>
A;Residues: 24-34 <SMU1>
A;Residues: 24-34 <SMU1>
B;Residues: 24-34 <SMU1>
B;Residues: 24-34 <SMU1>
B;Residues: 24-34 <SMU1>
B;Residues: 24-34 <SMU1>
J; Broadwell, A.H.
J; Gen. Microbiol. 138, 55-62, 1992
A;Fitle: Identification of an insecticidal crystal protein from Bacillus thuringiensis A;Reference number: A44847; WUID:92211329; FMID:1556556
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                   RKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPEIP 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIPN 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WNSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDDDTGVLSAD 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     996
                                                                                                                                                                                                                                                                                                                   DAKHRILDVSDNILPDILPENTCGEPNRCAAQQYLDENPSPRCSSMQDGILSDSHSPSLA 856
                                                                                                                                                                                                                                                                                                                                                                                   708
                                                                                                                  DVLPKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGPIGSSQDLEIKLIRH 826
                                                                                                                                                                                                                                                   827 RANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMSSDSHAFSFH 886
                                                                                                                                                                                                                                                                                                                                                                  IDTGEIDINENTGIWVVPKI PTTNGYATLGNIELVEEGPLSGETLERAQQQEQQWQDKMA 946
                                RLFVTISG-----TRIYSINVNKTMNKGDDLFPNTFDLATIGTAFTFSNYSDSLTVGADS 648
AVKMYKLDDPSTVVKGPGFTGGDLVKRGSTGYIGDIKATVNSPLSQKYRVRVRYATNVSG 561
                                                  CHAVINDKITLQTKPQ--NTVETIGEGKDLTYGSFGYIBYSTTIQFPDEHPKITLHLSD
                                                                                               FASGGEVYVDKFELIPVNATFEAEEDLDVAKKAVNGLFTSKKDALQTSVTDYQVNQAANL
                                                                                                                                                                VECLSDELYPNEKRMLWDAVKRAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHITETQALYTRAKQALDNI,PANAQDSHLKRDVTFARIAAARKIVQSIREAYMSWLSVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-1156 <SMU>
A;Cross-references: EMBL:X58120; NID:g870929; PIDN:CAA41122.1; PID:g40271
A;Experimental source: subsp. galleriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-1151 <GLB>
A;Cross-references: EMBL:X58534; NID:g48879; PIDN:CAA41425.1; PID:g48880
A;Experimental source: isolate DSIR517
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993 SIPYVYNDALPRIPGMNYTSPTRLTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVN 1052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEKCAHESHHFSLDIDVGCTDLNBDLDVWVIFKIKTQDGHARLGNLBFLEBKPLVGBALA 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAQQQBQQWQDKWARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQ 992
                                                                                                         580
                                                                                                                                                                                                                YRARIRYASTTNIRLFVTISGTRIYSINVNKTMNKGDDLJFNTFDLATIGTAFTFSNYSD 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G-NMSSDSHAPSPHIDTGEIDLNENTGINVVPKIPTTNGYATLGNLBLVEEGPLSGETLE 932
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C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Bacession: S32645
R;Lambert, B.
submitted to the EMBL Data Library, April 1993
A;Rcession: S32645
A;Rcession: S32645
A;Rcession: Lype: DNA
A;Accession: S2645
A;Status: preliminary
A;Accession: C;Accession: C;Acces
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                                                                                                                                      1112 TENIC----ADQTS----
TONYNTIDEIPPENBPLS - - RGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADV
                                                                                                         TWTVYSDKITQI PVVKAHTLVSGTTVI KGPGPTGGNI LKRTSSGPLAYTSVSVKSPLSQR
                                                                                                                                                                                                                                                                                                                          SLIVGADS PASGGEVYVDKFELI PVNATFEAREDLDVAKKAVNGLFTS - KKDALQTSVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                    700 YOVNQAANLVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRING--BNGWTG
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A;Residues: 11166 <LAM>
A;Cross-references: EMBL: Z22510; NID: g295861; PIDN: CAA80233.1; PID: g295862
C;Superfamily: parasporal crystal protein
C;Reywords: delta-endotoxin
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parasporal crystal protein crylFal - Bacillus thuringiensis (strain aizawai)
N;Alternate names: parasporal crystal protein crylF
C;Species: Bacillus thuringiensis
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 01-Dec-2000
C;Accession: A42459 #sequence_revision 10-Jul-1992 #text_change 01-Dec-2000
C;Accession: A42459
A;Title: Isolation and characterization of a novel insecticidal crystal protein gene fro
A;Accession: A42459
C;Accession: A42459
C;Coss-references: GB:M63897; NID:g142757; PIDN:AAA22348.1; PID:g142758
C;Coss-references: GB:M63897; NID:g142757; PIDN:AAA22348.1; PID:g142758
C;Coss-references: GB:M63897; NID:g142757; PIDN:AAA22348.1; PID:g142758
                                                                                                                                                                                                                                                                                                                                                       EWSDMLAAQNLVQSIPYVYNDALPEIPGMNYTSPTELTNRLQQAMNLYDLRNAIPWGDFR 1039
                                                                                                                                                                  NGLSDWNATSDVNVQQLSDTSVLVI PNWNSQVSQQFTVQPNYRYVLRVTARKBGVGDGYV 1099
                                                                                                                                                                                                                                                                            25;
                                                         59 NPRIPISSSTVQTG-----IGIVGQVLGALGVPPAGQIASFYSFIVGQLWPSSTVSVW 111
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                            LVERCPLSGETLERAQQQEQOWQDKWARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGV
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35.6%; Score 2154.5; DB 2;
Best Local Similarity 40.5%; Pred. No. 7.7e-117;
Matches 488; Conservative 185; Mismatches 390;
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Arabical crystal protein - Bacillus thuringiensis (strain aizawai)
C;Species: Bacillus thuringiensis
C;Baccies: Bacillus thuringiensis
R;Oceda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H
Gene 53, 113-119, 1987
A;Reference number: A26513; MUID:87248103; PMID:3297927
A;Reference number: A26513; MUID:87248103; PMID:3297927
A;Accession: A26513
A;Status: preliminary
A;Mesidues: 1-1155 <ORD>
A;Cross-references GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143099
C;Superfamily: parasporal crystal protein
C;Superfamily: parasporal crystal protein
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NyAlternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal procession statistic classics. Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 01-Dec-2000
C;Accession: A90025; A91560; A90555; S14555; A26461; A24172; A29043; JD0002
R;Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.
Agric. Biol. Chem. S1, 455-463, 1987
A;Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from A;Reference number: A90025
A;Molecule type: mRNA
A;Residues: 1-1155 <KON>
A;Residues: 1-1155 <KON>
A;Residues: 1-1155 <KON>
A;Residues: 1-1185 <KON = 1986
A;Title: The hypervariable region in the genes coding for entomopathogenic crystal prote A;Recession: A91560; MUID:8716355; PMID:3557124
A;Recession: A91560; MUID:87163505; PMID:3557124
A;Residues: 1-1155 <KGEI>
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A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thu
A;Reference number: A26461; MUID:87054026; PMID:3023091
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                                                                                                                                                     gene product ana
                                                                                                                                                                                                                                                               A; Molecule type: DNA .
A; Molecule type: DNA .
A; Residues: 1-1155 < WAB.
A; Cross-references: GB:M13998; NID:g142719; PIDN:AAA22330.1; PID:g142720
A; Experimental source: Bubsp. berliner
B; Chak, K.P.; Jen, J.C.
Bubmitted to the EMBL Data Library, October 1990
A; Description: Complete nucleotide sequence and expression in Bscherichia coli of A; Reference number: S14555
A; Accession: S14555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-710, L',732-784, R',786-1155 <HOP>
A;Cross-references: GB:X04698; NID:g40254; PIDN:CAA28405.1; PID:g40255
A;Experimental source: strain berliner 1715
c;Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
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A; Molecule type: DNA
A; Residues: 1-1155 < CHA>
A; Residues: 1-1155 < CHA>
A; Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
A; Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
R; Hofte, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe,
Eur. J. Biochem. 161, 273-280, 1986
A;Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:g143124
A;Experimental source: subsp. kurstaki
R;Wabiko, H:; Raymond, K.C.; Bulla Jr., L.A.
DNA 5, 305-314, 1986
                                                                                                                                             A;Title: Bacillus thuringlensis entomocidal protoxin gene sequence and A;Reference number: A90955; MUID:86300092; PMID:3743328
A;Accession: A90955
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C;Keywords: delta-endotoxin
F;82-386/Product: toxic peptide #status predicted
F;82-300/Region: toxic #status predicted
F;300-586/Region: insecticidal #status predicted
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J. Mol. Biol. 208, 183-194, 1989
A.Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid of A; Reference number: S04994; MUID:89362455; PMID:2769751
A; Accession: S04994
A; Molecule type: DNA
A; Residues: 429-449, A' 451-724 < HAW>
A; Residues: 429-449, A' 451-724 < HAW>
A; Cross-references: EMBL:X16315
A; Cross-references: EMBL:X16315
C; Comment: This toxin is lethal to the larvae of lepidopterans and dipterans. C; Superfamily: parasporal crystal protein
C; Superfamily: parasporal crystal protein
C; Keywords: delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                64 IWGIFGPSQ----WDAFLVQIEQLINQRIEEFARNQAISRLEGISNLYQIYAESFREWEA 119
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                                                                                                                                                                                      Length 1155;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                         DB 2;
                                                                                                                                                                                      Query Match 34.0%; Score 2052.5; DB 2; Best Local Similarity 39.4%; Pred. No. 6.3e-111; Matches 479; Conservative 183; Mismatches 388;
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S02134
parasporal crystal protein cryICl - Bacillus thuringiensis (strain aizawai ICl)
NyAlternate names: delta-endotoxin ICl; entomocidal crystal protein
C;Species: Bacillus thuringiensis
A;Variety: strain aizawai ICl
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C;Accession: S02134; S04994
R;Haider, M.Z.; Ellar, D.J.
Nucleic Acids Res. 16, 10927, 1988
A;Title: Nucleotide sequence of a Bacillus thuringiensis aizawai ICl entomocidal cry
A;Reference number: S02134; MUID:89083518; FMID:3205732
A;Recession: S02134; MUID:89083518; FMID:3205732
A;Reterence number: S02134; NID:940277; PIDN:CAA31620.1; PID:940278
A;Reserences: EMBi:X13233; NID:940277; PIDN:CAA31620.1; PID:940278
A;Experimental source: strain aizawai ICl
R;Haider, M.Z.; Ellar, D.J.
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                     ARYGNLPVFAWTHRSADVTNTVYSDKITQIPVVKAHTLVSGTTVIKGPGPTGGNILKRTS
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	Procession: 1970-1970-1970-1970-1970-1970-1970-1970-	OY 218 AEWGFPGEISTFYDROVTRIAQYSDYCVKWYNTGLDKLKGTNAASMLKYHOPRREMTLL 277

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A;Accession: JC2219
A;Aolcoule type: DNA
A;Rolcoule type: DNA
A;Residues: 1-1176 (UDA>
A;Crosa-references: DDBJ:D17518; NID:g506190; PIDN:BAA04468.1; PID:g535781
C;Genetics:
A;Gene: cry1A(a)
C;Superfamily: parasporal crystal protein
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
                                                                                                                                                                                                                                         NRNDTRARSVVVTQYIALELDFVAKIPSFAISGQEVPLLSVYAQAANLHILLIRDASIFG
                                                                                                                                                                                                                                                                                     AEMGPTPGE ISTPYDROVTRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHOPRREMTLL
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                                                                                                                                                NPEL------FGNPET-PISSSTVQTG---IGI----VGQVLGALGVPPAGQIASPYSP
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                                                                                                   Query Match 33.8%; Score 2045; DB 2; Length 1176; Best Local Similarity 39.3%; Pred. No. 1.8e-110; Matches 479; Conservative 174; Mismatches 415; Indels 152;
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parasporal crystal protein cryAel - Bacillus thuringiensis (strain alesti)
C;Species: Bacillus thuringiensis
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 01-Dec-2000
C;Accession: A41052
Bacteriol. 173, 6615-6618, 1991
A;Title: Cloning and analysis of delta-endotoxin genes from Bacillus thuringiensis subs;Accession: A41052
A;Accession: A41052
A;Cossion: A41052
A;Cossion
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GTITSNKIKYYDLANKDIPQVRSLGADLANYYAQ--VYGVPYASFTLLDKNT----GSGS
                                                                                                                                                  OKLINSGVEMSDMLAAQNLVQSIPYVYNDALPEIPGMNYTSFTELTNRLQQAWNLYDLRNA
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A29125
paragoral crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)
C;Species: Bacillus thuringiensis subsp. kurstaki
C;Oste: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 01-Dec-2000
C;Accession: A29125
B;Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme Bio/Technology 5, 807-813, 1987
A;Fitle: Insect tolerant transgenic tomato plants.
A;Reference number: A29125
A;Accession: A29125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGDFRNGLSDWNATSDVNV-QQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKEG 1093
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   GTMGNAAPQQRIVAQLGQGVYRTLS---STPYRNPFIIGINNQRLSVLDGTBPAYGSSSN 395
                                                                                                                                                                                                                 NALFTSPNQIGLKTDVTDYHIDQVSNLVBCLSDBFCLDBKRELSBKVKHAKRLSDBRNLL
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                                                                                                                  ARYGNLPVPAWTHRSADVTNTVYSDKJTQIPVVKAHTLVSGTTVIKGPGPTGGNILKRTS
                                                                                                                                      IR---APMPSWIHRSABPNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTS
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Search completed: June 21, 2004, 13:39:44 Job time: 34 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 21, 2004, 13:31:10 ; Search time 17 Seconds (without alignments) 3574.463 Million cell updates/sec

US-10-089-678-1 6044 1 MSPNNQNBYBILDASSSTSV......MSBTEGVFNIBSVELVLRBE 1167 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	a	CBAA BACUK	C8CA_BACTP	C8BA_BACUK	C9CA_BACTO	C9RA_BACTA	C9DA_BACTP	C1KA_BACTM	C1BB_BACTU	C1BA_BACTK	C1BC BACTM	C1BE_BACTU	C7AA_BACTU	C7AB_BACUA	C1BD_BACTZ	C7AB_BACUK	COAA_BACTF	C9AA BACTG	C1FA_BACTA	C1GA_BACTU	CLJA BACTU	C1JB_BACTU	CLAB BACTK	CLAE_BACTL	CLAA BACTK	C1EA_BACTX	C1AD_BACTA	CIGB_BACTZ	C1CA_BACTE	C1FB_BACTM	CIDB BACTU	C1EB BACTA	C1DA BACTA	CLAC_BACTK
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	Score	4007	3733.5	3152	3123	2825.5	~	2714	N	2547.5	2491	2462	2458.5	2458.5	2445	2439.5	2227.5	2191	2154.5	2093.5	2065.5	2065	2061.5	2044.5	2038	2024.5	2011.5	1999	1995	g,	1953.5	1946.5	94	1939
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ALIGNMENTS

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                                                                                                659 KPELIPVNATPEAEEDLDVAKKAVNGLPTSKKDALQTSVTDYQVNQAANLVECLSDELYP 718
                     181 AKIPSFAISGQEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTFGEISTFYDRQVTRTAQ 240
                                                                              SSIPSPAVSGHEVILLIAVYAQAVNIHILILRDASIFGEEMGFTPGEISRFYNRQVQLTAE 240
                                                                                                                                                         LPLANNTEYLEYWYCHSIKYKNT-NASSALERNYGTITSNKIKYYDLANKDIFQVRSLGAD 419
                                                                                                                                                                 LANYYAQVYGVPYASFTLLDXXNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPPENE-P 478
                                                                                                                                                                                              LSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWIHRSADVTNTVYSDKITQIPVVKAH 538
                                                                                                                                                                                                                          TLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSGRYRARIRYASTTNLRLFVT 598
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              ETPISSSTVQTGIGIVGQVLGALGVPPAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVED 120
                                          LIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALBLDFV 180
MSPNNONEYEIIDATPSTSVSSDSNRYPPANEPTDALONMNYKDYLKMSGGENPELPGNP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCATABORIA DECLIES.";
J. Appl. Bacteriol. 76:307-313(1994).
-!- FUNCTION: PROMOTES COLLOIDGEMOTIC LYSIS BY BINDING TO THE MIDGUT
-!- FUNCTION: PROMOTES COLLOIDGEMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF INSECTS. A. RUPGUTER ON VARIOUS SCARABABID BEBTLES
SUCH AS ANOMALIA CUPREA, A. RUPGUTERA AND POPILLIA JAPONICA.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a novel crystal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sato R., Takeuchi K., Ogiwara K., Minami M., Kaji Y., Suzuki N., Hori H., Asano S., Ohba M., Iwahana H.;
"Cloning, heterologous expression, and localization of a novel crye protein gene from Bacillus thuringiensis serovar japonensis strain buibui toxic to scarabaeid insects.";
[Curr. Microbiol. 28:15-19(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the spore coat.
MISCELLANDOUS: Toxic segment of the protein is located in the
                                                                                                                                                                                                                                                                                                                                                                                             Pesticidial crystal protein cry8Ca (Insecticidal delta-endotoxin
CryVIIIC(a)) (Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-14 AND 56-64, AND CHARACTERIZATION.
MEDLINE=94259659; PubMed=8200856;
Hori H., Sturki N., Ogiwara K., Himejima M., Indrasith L.S.,
Wilnami M., Asano S., Sato R., Obba M., Iwahana H.;
"Characterization of larvicidal toxin protein from Bacillus
thuringienels serovar japonensis strain Buibui specific for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indele
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64.2%; Pred. No. 4.4e-205;
ive 109; Mismatches 257;
                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein crysca (Insecticida)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis (subsp. japonensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
NCBI_TaxID=128936;
1139 PSTEQUWIDMSETECVFNIESVELVLREE 1167
| |:|:||::|||| | |||||::|
1129 PYTDQMWIEISETEGTFYIESVELIVDVE 1157
                                                                                                                                                                                                                               PRT; 1160 AA
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PIR; I40589; I40589.
HSSP; P07130; DLC.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR008979; endotoxin.N.
InterPro; IPR08979; Gal.bind_like.
Pfam; PP00555; endotoxin.1.
Pfam; PP03944; endotoxin.C; 1.
Pfam; PP03945; endotoxin.C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94100786; PubMed=7764305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRYBCA OR CRYVIIIC(A) OR CRYIII.
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SEQUENCE FROM N.A.
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Best Local Simi
Matches 767;
                                                                                                                                                                                                                                  BACTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein)
                                                                                                                                                                                                                                                          045706;
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CSCA_BACTP
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                                                                                                                                                                         Bacillus thuringiensis (subsp. kumamotoensis).
Bacteria: Pirmicutes; Bacillales; Bacillaceae;
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InterPro; IPR005638; endotoxin_C.
InterPro; IPR0086539; endotoxin_N.
InterPro; IPR008979; Gal_bind_Tike.
Pfam; PP00555; endotoxin; 1.
Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endotoxin_N; 1.
                                                                                                                                                                                                                                                           number WO9315206, 05-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1169 AA; 133543 MW;
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                                                                                          STANDARD;
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SEQUENCE 1169 AA;
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RINMGSPSQTNYETPILPTYAQAASLHILVWRDVQIYGKEWGYPQNDIDLFYKEQVSYTA
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                                    RTFISS-STVQTGIGIVGQVLGALGVPPAGQIASFYSFIVGQLMPSSTVSVWEMIMKQVB
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
ETPIS-SSTVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLMPSSTVSVWEMIMKQVB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSPNNONEYBILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELPGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- MISCELLANEOUS: Toxic segment of the protein is located in the
                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry8Ba (Insecticidal delta-endotoxin Cry1IB(a)) (Crystaline entomocidal protoxin) (134 kDa crystal protein).
CRYBBA OR CRYVIIB(A) OR 50C(B).
                                                                                                                          84;
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                                                                                                     QLTREVYTDPIVFNRETSGGFCRRWSLNSDISFSBVBSAVIRSPHLFDILSBIBFYTTRA 359
                                                                                                                                             GLPLNNTEYLEYWVGHSIKYKNTNASSALRRNYGT----ITSNKIKYYDLANKDIFQVR 414
                                                                                                                                                               S--FTSDRYMRYWAGHQISYKHIGTSSTFTQMYGTNQNLQSTSN----FDFTNYDIYKTL 410
                                                                                                                                                                                     SLGADLAN-----YYAQVYGVPYASFTLLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTI 469
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ELINQKIAEYARNKALSELEGLGNNYQLYLTALEEWKENPNGSRALRDVRNRFBILDSLF 180
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

A EMBLINE-95144404; PubMed=8572715;

A Becillus thuringienels insecticidal crystal protein with a high activity against members of the family Noctuidae.";

A Bacillus thuringienels of the family Noctuidae.";

A Pacillus thuringienels of Lef family Noctuidae.";

A PATIVITALIAL CELLS OF LEPIDOPTERA LARVAE. HAS A FAIRLY BROAD SEPTRALIDAE, SPETRUM OF ACTIVITY AGAINST MEMBERS OF THE FAIR PRABLIDAE,

PLUTELLIDAE, SPHINGIDAE, AND NOCTUIDAE. IT IS THE PIRST

C INSECTICIDAL CRYSTAL PROTEIN WITH ACTIVITY ACAINST CUTWORMS. NO

C ACTIVITY IS OBSERVED AGAINST SOME BERTLES, SUCH AS COLORADO POTATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the spore coat.
                                                       30-MAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
16-OCT-2000 (Rel. 40, Last annotation update)
Pesticidial crystal procesin cry9Ca (Insecticidal delta-endotoxin CryIXC(a)) (Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424
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SEQUENCE 1157 AA; 129775 MW; C364391EF7FDFBBA CRC64;
                                                                                                                                                                                                                                                                                              Bacillus thuringiensis (subsp. tolworthi).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
NCBI_TaxID=1442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the delta endotoxin family.
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52.3%; Pred. No. 2.8e-170;
ive 195; Mismatches 327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 52.3%; Pre
Matches 619; Conservative 195;
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InterPro; IPR001178, Endotoxin.
InterPro; IPR005638; endotoxin.
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STANDARD;
                                                                                                                                                                                                                               protein).
CRY9CA OR CRYIXC(A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         terminus
C9CA BACTO
045733;
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                                                                                                  QYSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMILLVLDLVALPPNYDTRTYPIETTA 299
                                                                                                                                                                                                                    GLPLNNTEYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKY---YDLANKDIPQVRSL 416
                                                                                                                                                                                                                                   360 -PPV-SSNFMDYWSGHTLRRSYLNDSAVQEDSYGLITTTRATINPGVDGTWR----IRST 413
                                                                                                                                                                                                                                                                                                         461
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                                                                                                                                                                                                                                                                            GADLANYYAQVYGVPYASFTL--LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP.
                                                                                                                                                                                                                                                                                                      414 AVDFRSALIGIYGVNRASFVPGGLFNGTTSPANGG------CRDLYDTNDELPP
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                                          VAKIPSPAISGOEVPLLSVYAQAANLHLLLLRDASIPGAENGPTPGEISTFYDRQVTRTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 RIYPIBITAQLIREVYIDPIVFNRBISGGFCRRWSLNSDISFSBVBSAVIRSPHLFDILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTTLQNMNYKDYLRMSBGB-----NP
                                                                                                                                                                                                                                          Bacillus thuringlensis cry gene for insecticidal crystal protein."; submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                      the spore coat. MISCELLANBOUS: Toxic segment of the protein is located in the N-
                                          16-OCT-2001 (Rel. 40, Last sequence update)
6-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry9Ea (Insecticidal delta-endotoxin CryIXE(a)) (Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                                        EPITHELIAL CELLS OF INSECTS.
DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 46.7%; Score 2825.5; DB 1; Length 1150; Best Local Similarity 48.6%; Pred. No. 2.6e-153; Matches 574; Conservative 197; Mismatches 364; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1150 AA; 129895 MW; 7D6AB93D6BDC97BB CRC64;
                                                                                                                                  Bacillus thuringlensis (subsp. aizawai).
Bacteria, Pirmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1433;
                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the delta endotoxin family.
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InterPro; IPR001178; Endotoxin.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal_bind_like.
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Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endotoxin_N; 1.
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                              16-OCT-2001 (Rel. 40, Created)
 STANDARD;
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                                                                                                                    CRY9EA OR CRYIXE (A)
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                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=SSK-10;
                                                                                                                                                                                                                                                                                                                                                                       terminus.
C9EA BACTA
Q9ZNL9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIN--LRLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGAD 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISFVVNLFVNNSAA---GFTLPSTMAQNGSLTYESFNTLEVTHTIRFSQSDFTLKLAIF 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVEEGPLSGETLERAQQQEQQWQDKM 945
                                                                                                       RLTISRNRYTAPTTNS-PLDYWSGHTLQSQHANNPTTYBTSYGQITSN-TRLENTTN-GA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the RMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

EMBL; D85560; BAA19948.1; -. HSSP; P07130; IDLC.

-!- SIMILARITY: Belongs to the delta endotoxin family.

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Asano S.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT BPITHELIAL CELLS OF INSECTS.
-!- DEWELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part che spore coat.
-!- MISCELLANBOUS: Toxic segment of the protein is located in the N--

FROM N.A.

SEQUENCE

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408
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                                                                                                                                                                                        46;
                                                                                                                                                         Length 1169;
                                                                                                                                                       Query Match

44.9%; Score 2715; DB 1; Length 11
Best Local Similarity 46.9%; Pred. No. 5.3e-147;
Matches 558; Conservative 204; Mismatches 383; Indels
                                                                                                                            1169 AA; 132228 MW; 659AB257229DE5B9 CRC64;
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InterPro; IPR005639; endotoxin.C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PR00555; endotoxin, 1.
Pfam; PP03944; endotoxin, C; 1.
Pfam; PP03945; endotoxin_N; 1.
                                                                                                               Toxin; Sporulation
SEQUENCE 1169 AA
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry9Da (Insecticidal delta-endotoxin CryIXD(a)) (Crystaline entomocidal protoxin) (132 kDa crystal

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BACTP

C9DA BAC 006014;

protein). CRY9DA OR CRYIXD(A). Bacillus thuringiensis (subsp. japonensis). Bacteria; Firmicutes; Bacillales; Bacillus

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U28801; AAB00376.1; -. P02965; ICIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toxin; Sporulation.
SEQUENCE 1215 AA;
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"Cloning of a novel crystal protein gene crylk from Bacillus
thuringiensis subsp. morrisoni."

FERS Microbiol. Lett. 134:159-164(1995).

-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
BITHELIAL CELLS OF INSECTS. SELECTIVELY TOXIC TO ARTOGEIA RAPAE
AND NOT ACTIVE ON PUTFELLA XYLOSTELLA.

-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                      DLEIDLIHYHKVHLVKNVPDNLVSDTYSDGSCSGMNRCEBQQMVNAQLETEHHHPMDCCB
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                                                             YRARIRYASTTNLRLFVTISGTRIYSINVNKT#NKGDDLTFNTFDLATIGTAFTFSNYSD
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                                           TWIVYSDKITOIPVVKAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSQR
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30-WAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystaline protein crylka (Insecticidal delta-endotoxin
CCYIK(a)) (Crystaline enconcidal protoxin) (137 kDa crystal protein)
CRYIKA OR CRYIK(A) OR CRYIK.
Bacillus thuringiensis (subsp. morrisoni).
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SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 RACLPLANTEYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKYYDL--ANKDIFQVRS
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                       is located
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    -!- SIMILARITY: Belongs to the delta endotoxin family

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
44.9%; Score 2714; DB 1;
Best Local Similarity 46.3%; Pred. No. 6.4e-147;
Matches 581; Conservative 194; Mismatches 351;
the spore coat.
MISCELLANBOUS: Toxic segment of the protein
                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR0086539; endotoxin_N.
InterPro; IPR008979; Gal_bind_Tike.
Pfam; PP00555; endotoxin, 1.
Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endotoxin_N; 1.
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EMBL; L32020; AAA22344.1;
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                                                                                                                                                                                                                                                                           PGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIP 1065
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                    684
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30-MAY-2000 (Rel. 39, Last sequence update)
Pesticidial crystal 39, Last annotation update)
Pesticidial crystal protein crylBb (Insecticidial delta-endotoxin CrylBb(b)) (Crystaline entomocidal protoxin) (140 kDa crystal protein).
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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                                                                                        KORSLRLTSARRIDTETYPTYLYQQIDBSLLKPYTRYKLKGPIGSSQDLRIKLIRHRANQ
                                                                                                          KENYVELPGT--VD-ECYPTYLYQKIDESQLKSYTRYQLRGYIEDSQDLEIYLIRYNAKH
                                                                                                                                                    EVYVDKFELI PVNATPEAEEDLDVAKKAVNGLPTSKKD-ALOTSVTDYQVNQAANLVECL
            SDBLYPNEKRMLWDAVKBAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVAEGDVLF
                                                                                                                                     IVKNVPDNLLP----DVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMS-SDSHAFSF
                                                                                                                                                                                                                                                    920 EKLOLETKRVYTEAKESVDALFVDSOYDKLOANTNIGIIHGADKOVHRIREPYLSELPVI
                                                                                                                                                                                                                                                                                                                         NWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFN-----
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"Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
toxic to lepidopteran insects".

Patent number US5322687, 21-JUN-1994.

-!- PUNCTION: PROWOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
BETTHELIAL CELLES OF MANY LEPIDOPTERAN LARVAE.

-!- DEVELOPMENTAL STRAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the spore coat.
MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                                                   ----YITKTVEFTPSTEQVWIDMSETEGVFNIESVELVLEEE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                402 AGTNILPTTPVNGVPWARPNPINPQ-NIYERGATTYSQPYQGVGI--QLFDSBTBLPPBT
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Indels 140;
                                                                                                                                                                                                                                                                                                                                              Length 1229;
                                                                                                                                                                                                                                                                                                  A4C949DB675C3269 CRC64;
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                                                                                                                                                                                                                                                                                                                                          Query Match 42.2%; Score 2552; DB 1;
Best Local Similarity 43.2%; Pred. No. 1.1e-137;
Matches 548; Conservative 205; Mismatches 375;
                                                                                                                                     InterPro; IRR001178; Endotoxin.
InterPro; IRR005639; endotoxin.C.
InterPro; IRR005639; endotoxin.N.
InterPro; IRR008979; Gal_bind_like.
Pfam; PP00555; endotoxin.1.
Pfam; PP03944; endotoxin.C; 1.
Pfam; PP03945; endotoxin.N; 1.
                                                                                                                                                                                                                                                                                 Toxin; Sporulation.
SEQUENCE 1229 AA; 139769 MW;
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us-10-089-678-1.rsp

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1105
                                                                                                                                                                                                                                                                                                             -----YITKTVEPTPSTEQVWIDMSBTEGVFNIES 1159
 810
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DEVELOPMENTAL STARS: The crystal protein is produced during sportlation and is accumulated both as an inclusion and as part of
                                                                         -ENGWIGSTGIEVARGDVLPKDRSLRLTSARRIDTETYPTYLYQQIDESLLKPYTRYKLK
                GFIGSSQDLEIKLIRHRANQIVKNVP--DNLLPDVL--PVNSCGGIDRCSEQQYVDANLA
                                                                                                                LENNGENG-MASSDSHARSFHIDTGEIDLNENTGIWVVPKIPTTNGYATLGNLELVBEGP
                                                                                                                              LDCSCRDGERCAHHSHHFTLDIDVGCTDLHENLGVWVVFKITTQEGYARLGNLEFIEBRP
                                                                                                                                                                          LSGETLERAQQQEQQWQDKWARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDML
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                                                                                                                                                                                                                                                                                            NATSDVNVQQLSDTSVLV1PNWNSQVSQQPTVQPNYRYVLRVTARKBGVGDGYV1IRDGA
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01-NOV-1988 (Rel. 09, Created)
01-REB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 33, Last annotation update)
920-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein crylBa (Insecticidal delta-endotoxin CrylB(a)) (Crystaline entomocidal protoxin) (140 kDa crystal protein)
CRYIBA OR CRYIB(A) OR CRYA4.
Bacillus thuringiensis (subsp. kurstaki), and
Bacillus thuringiensis (subsp. entomocidus).
Bacteria; Firmicutes; Bacillales; Bacillus.
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Brizzard B.L., Whiteley H.R.;
Nucleotide sequence of an additional crystal protein gene cloned
from Bacillus thuringiensis subsp. thuringlensis.";
Nucleic Acids Res. 16:2723-2723(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the spore coat. MISCELLANEOUS: Toxic segment of the protein is located in the
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Soetaert P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=B.t.kurstaki; STRAIN=HD-2;
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SIMILARITY: Belongs to the delta endotoxin family

terminus

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42.1%; Score 2547.5; DB 1; Length 1228;
Best Local Similarity 43.8%; Pred. No. 2e-137;
Matches 558; Conservative 183; Mismatches 381; Indels 151;
                                                                                                                                                                                                                                                                                                   -> H (IN STRAIN HD-110).
C8E3A19PB5D98575 CRC64;
                                                                                                                                             PIR, 500873; S00873.
HSSP, P07130; IDLC.
INTERPO; IDRO1178; Endotoxin.
InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR008979; endotoxin.N.
Pfam; PP00555; endotoxin, 1.
Pfam; PP03944; endotoxin, 1.
Pfam; PR03944; endotoxin, 1.
Toxin; Sporulation.
VARIANT 150 150 Y -> H (I
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1228 AA; 139647 MW;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last amonotation update)
Pesticidial crystal protein crylBc (Insecticidal delta-endotoxin CrylB(c)) (Crystaline entomocidal protoxin) (140 kDa crystal protein).
CRYIB(C)) (CRYIB(C) OR CRYIBC.
Bacillus thuringlensis (subsp. morrisoni).
Bacteria, Firmicutes; Bacillales; Bacillus.
                                                           ECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRIN------
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"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
Submitted (NUV-1994) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: PROWOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT BETHERLALL CELLS. OP INSECTS.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part (
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MISCELLANEOUS: Toxic segment of the protein is located in the N-
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content
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                                                                                                                                                                                                                Query Match
41.2%; Score 2491; DB 1;
Best Local Similarity 42.1%; Pred. No. 3.4e-134;
Matches 536; Conservative 208; Mismatches 384;
 use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See Por
or send an email to license@ieb-sib.ch).
                                                                                    InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR008979; endotoxin_N.
InterPro; IPR008979; endotoxin_N.
Pfam; PP00555; endotoxin_1.
Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endotoxin_N; 1.
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                                                               EMBL; 246442; CAA86568.1;
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                                                                                                                                                                                                                                                                       986 AAQNLVQSIPYYYNDALPBIPGMOYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDW 1045
                                                                                                                                                                                                                                                                                         NATSDVNVQQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGA 1105
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                                                                                   EPITHELIAL CELLS OF WANY LEPIDOPTERAN LARVAE.
DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
-ENGWTGSTGIBVAEGDVLFKDRSLRLTSARBIDTBTYPTYLYQQIDESLLKPYTRYKLK
                   GPIGSSODLEIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQ----YVDANLA
                                                                                                                                                                                                    L.SGETLERACCOGECOWODKWARKRGASEKAYYAAKQAIDRLFADYQDCKLNSGVEMSDML
                                                                                                                                    LENNGENG-NMSSDSHAFSFH1DTGB1DLNRNTG1WVVFK1PTTNGYATLGNLELVEBGP
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 CRAL 40, Last annotation update)
Pesticidial crystal protein crylBe (Insecticidal delta-endotoxin
CrylB(e)) (Crystaline encomocidal protoxin) (139 kDa crystal protein)
CRY1BE OR CRYIB(B) OR 158C2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=NRRL B-18872 / PS158C2;
Payne J.M., Cummings D.A., Cannon R.J.C., Narva K.E., Stelman S.;
"Bacillus thuringiensis genes encoding lepidopteran-active toxins.";
Patent number US5723758, 03-MAR-1998.
-i- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the spore coat.
MISCELLANEOUS: Toxic segment of the protein is located in the N-
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1222 IVDSVELLEMBE 1233
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                                                                                                                                                                                     Indels 134;
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                                                                                                                                   CBA847BEA0B34CD3 CRC64;
                                                                                                                                                           Query Match 40.7%; Score 2462; DB 1;
Best Local Similarity 42.9%; Pred. No. 1.5e-132;
Matches 542; Conservative 196; Mismatches 392;
                                InterPro; IPR005139; Endotoxin.
InterPro; IPR005639; endotoxin C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal bind like.
Pfam; PP00555; endotoxin; 1.
Pfam; PP03944; endotoxin C; 1.
Pfam; PP03945; endotoxin N; 1.
Toxin; Sporulation; Plasmid.
                                                                                                                                   139084 MW;
          AAC32850.1;
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P07130; 1D
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                                                                                                                                                           LVQSIPYVYNDALPRIPGMNYTSFTELTWRLQQAWNLYDLRNAIPNGDFRNGLSDWNATS 1049
                                                                                                                                                                                                               1050 DVNVQQLSDISVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTE 1109
                                                                             923
                                                                                                                    MEDLINE=92384571; PubMed=1514800;
MEDLINE=92384571; PubMed=1514800;
Lambert B., Hofte H., Annys K., Jansens S., Soetaert P., Peferoen M.;
Lambert Bacillus thuringiensis insecticidal crystal protein with a
silent activity against coleopteran larvae.";
Appl. Environ. Microbiol. 58:2536-2542(1992).
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
-EPITHELIAL CELLS OF COLEOPTERA. THIS PROTEIN IS NOT TOXIC IN ITS
NATURAL PORM. IT IS HIGHLY TOXIC TO COLORADO POTATO BEETLE LARVAE
AFTER AN IN VITRO SOLUBILIZATION AND TRYPSIN ACTIVATION STEP.
-!- DEVBLOPMENTAL STAGE: The crystal protein is produced during
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                                                                   CRDGEKCAHHSHHPSLDIDVGCIDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGE
                                                                                                       930 TLERAQQQEQQWQDKWARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQN
                                                                                                                                                                           SSODLEIKLIRHRANQIVKNVP--DNLLPDVL--PVNSCGGIDRCSEQQYVDANLALENN
                       DSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCA--PHFEWNPDLDCS
                                                     GENG-NMSSDSHAPSPHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVEEGPLSGE
                                                                                                                                                                                                                                                                                             1104 BLKFKNCBBEEVYPTDTGTCNDYTAHQGTAACNSRNAGYEDAYEVDTTASVNYKPTYBEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry7a (Insecticidal delta-endotoxin CryVIIA(a)) (Crystaline entomocidal protoxin) (129 kDa crystal
                                                                                                                                                                                                                                                                     ---ADOTS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus thuringiensis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
NCBI_TaxID=1428;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AKIPSPAISGOEVPLLSVYAQAANLHLLLLRDASIPGAEWGFTPGEISTFYDRQVTRTAQ
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                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                   1138 AA; 129391 MW; 69D8676D4F6A1FAC CRC64;
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                                                                                                                                                                                                                                                                          DB 1,
                                                                                                                                                                                                                                                                        40.7%; Score 2458.5; DB 1; ilarity 43.5%; Pred. No. 2.2e-132; Conservative 208; Mismatches 400;
                                                                                           InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PR00555; endotoxin; 1.
Pfam; PR03944; endotoxin_C; 1.
                                                                                       endotoxin C.
                                                                                                                                                                              Pfam; PF03945; endotoxin_C; 1.
Toxin; Sporulation.
SEQUENCE 1138 AA: 129491 MMP.
EMBL; M64478; AAA22351.1;
EMBL; A07236; CAA00646.1;
PIR; A48944; A48944.
HSSP; P07130; 1DLC.
                                                                           InterPro; IPR001178;
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Toxin; Sporulation.
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                                                                                                      947 RKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPEIP 1006
                                                                                                                                                                  WNSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDDDTGVLSAD 1126
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                     DAKHRILDVSDNILPDILPENTCGEPNRCAAQQYLDENPSPECSSMQDGILSDSHSPSIN 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Payme J.M., Fu J.M.;

"Coleopteran-active bacillus thuringiensis isolates and genes encoding coleopteran-active toxins.",

Patent number US2286486, 15-FEB-1994.

-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF COLDOPTERA.

-!- DEVELOPMENTAL STACE: The crysteal protein is produced during sporulation and is accumulated both as an inclusion and as part of
         RANQIVKNVPDNILEPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGENGSDSHAFSFH
                                                                     I DTGE I DLNENTG I WVVFKI PTTNGYATLGNLELVEEGPLSGETLERAQQQEQQWQDKMA
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                                                                                                                                                                                                                                                                                                                                                                      (Rel. 40, Last sequence update)
(Rel. 40, Last anoctation update)
crystal protein cry7Ab (Insecticidal delta-endotoxin
(Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                 1096 ISGYITKELEPPDTEKVHIRIGETEGIFLVESIELFLARE 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus thuringiensis (subsp. dakota).
Bacteria; Pirmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=132268;
                                                                                                                                                                                                                                                  1127 QTSYITKTVEFTPSTEQVWIDMSBTEGVPNIBSVELVLEBE 1167
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InterPro; IPR005639; endotoxin_N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PF00555; endotoxin_1.
Pfam; PF03944; endotoxin_C; 1.
Pfam; PF03945; endotoxin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001178; Endotoxin.
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                                                                                                                                                                                                                                                                                                                                     STANDARD;
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CRY7AB OR CRYVIIA(B)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 YKAFSHRIQPDLFYWCVHKVSFKKSBQSNLYTTGIYGKTSGYISSGAYSFRGNDIYRTLA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGADLANYYAQVYGVPYASPTLLDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTIDBIPPB 475
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                                                                                                           1 MSPNYQNBYBILDASSSTSVSDNSVRYPLANDQTTTLQNWNYKDYLRMSEGENPELPGNP
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                                                                         75; Gaps
                                     Length 1138;
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01DF7072C074CB88
                                     DB 1;
                                 tch 40.7%; Score 2458.5; DB 1; al Similarity 43.1%; Pred. No. 2.2e-132; 512; Conservative 218; Mismatches 384;
129778 MW;
1138 AA;
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1033 NGDFNNGLSCWNVKGHVDVQQSHHRSDLVIPEWRAEVSQAVRVCFGRGYILRVTAYKBGY 1092
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         AGTNILFTTPVNGVPWARPNFINPQ-NIYERGATTYSQPYQGVGI--QLFDSBTELPPBT 458
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                                                                                                                                                                                               YSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLLVLDLVALPPNYDTRTYPIETTAQ 300
                                                                                                                                                                                                                                                            LTREVYTOPIVPNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSEIBFYTTRAG 360
                                                                                      --IVGARNFSANAEVIIDRPEPIPVTATFEAEYDLERAQKAVNALFTSTNPRRLKTDVTD
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                                                                    LIDOKITDSVRKTALAGLOGLGDGLDVYQKSLKKWIENRNDTRARSVVVTQYIALBLDFV
                                                                                                                                 181 AKIPSPAISGOEVPLLSVYAQAANLHILLIRDASIPGAEWGFTPGEISTFYDRQVTRTAQ
                                                                                                                                                   TAIPLFRIRNEEVPLLMVYAQAANLHLLLLRDASLFGGSEWGMASSDVNQYYQEQIRYTEE
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                               999 NDALPEIPGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSD 1058
                                             26;
TKWRNKLAQMTTETQAIYTRAKQALDNLFANAQDSHLKIDVTFABIAAARKIVQSIREVY 968
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                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Pesticidial crystal protein crylBd (Insecticidal delta-endotoxin
CrylBdd)) (Crystaline entomocidal protoxin) (140 kDa crystal protein).
CRYIBD OR CRYIB(D) OR CRYLAI OR CRYEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                          TSVLVI PNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MS PNNONEYE I LDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=HD-525;
MEDLINE=20153386; PubMed=10688690;
Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.;
"Cloning of two new cry genes from Bacillus thuringlensis subsp.
                                                                                                                                                                      DTGVLSADQTSYITKTVEFTPSTEQVWIDMSETEGVFNIESVELVLEEE 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUIT. Microbiol. 40,227-232(2000).
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE PEPITHELIAL CELLS OF LEPIDOPTERAN LARVAE. TOXIC TO PLUTELLA XYLOSTELLA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1231 AA; 139654 MW; 129A0371CDDBEE52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           Bacillus thuringiensis (subsp. wuhanensis).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=52024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                terminus. SimilaRITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.5%; Score 2445; DB 1; 42.0%; Pred. No. 1.4e-131;
                                                                                                                                                                                                                                                                  1231 AA
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Interpro; IPR005638; endotoxin C.
Interpro; IPR005639; endotoxin N.
Interpro; IPR008979; eal bind like.
Pfam; PF00555; endotoxin; 1.
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PF03945; endotoxin_N; 1.
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                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toxin; Sporulation.
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Best Local Simil
Matches 537; C
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GASEKAYYAAKQAIDRLPADYQDQXINSGVEMSDMLAAQNLVQSIPYVYNDALPEIPGMN 1009
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                                                                 LIDOKITDSVRKTALAGLOGLGDGLDVYOKSLKNWLENRNDTRARSVVVTQYIALBLDFV
                                                                                                                     LIREVYTOPIVPMRETSGGFCRRWSLMSDISFSBVESAVIRSPHLFDILSEIEFYTTRAG
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NT-----AINTVVSVTGATLSALGVPGASPITNFYLKITGLLMPHDK-NIWDEPMTBVBT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                          ETFISSSTVQTGIGIVGQVLGALGVPPAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVED 120
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                                                                                         ---YITKTVEFTPSTEQVWIDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Payne J.M., Fu J.M.;
"Coleopteran-active Bacillus thuringiensis isolates and genes encodir coleopteran-active toxins.";
Patent number US5286486, 15-FEB-1994.
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT BENTHELIAL CELLS OF COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the spore coat.
MISCELLANEOUS: Toxic segment of the protein is located in the N-
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                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry7Ab (Insecticidal delta-endotoxin CryVIIA(b)) (Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.4%; Score 2439.5; DB 1; Length 1138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus thuringiensis (subsp. kumamotoensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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Interpro; IPR005438; endotoxin_C.
Interpro; IPR005639; endotoxin_N.
Interpro; IPR008979; Gal_bind_like.
Pfam; PF00555; endotoxin; 1.
                                                                                                                                                                     Pfam; PF03944; endotoxin_C; 1. Pfam; PF03945; endotoxin_N; 1.
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CRY7AB OR CRYVIIA(B)
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SEQUENCE 1138 AA;
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Search completed: June 21, 2004, 13:37:53 Job time: 23 secs

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SEQUENCE FROM N.A.

STRAIN-SDS-502;
Asanoto S., Yanamoto T.;
Asanot S., Yanamoto T.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
E. Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
REGL; AB089299; BAC07226.1; -.
GO; GO:0006952; Padc7226.1; -.
R GO; GO:0006952; Padcfense response; IRA.
R InterPro; IPR001178; Endotoxin. C.
R InterPro; IPR006503; endotoxin. C.
R InterPro; IPR006503; endotoxin. C.
R InterPro; IPR006503; endotoxin. C.
R InterPro; IPR008979; Gal_bind_like.
R Fam; PP00394; endotoxin. 1.
R Ffam; PP01394; endotoxin. N; 1.
SEQUENCE 1144 AA; 128060 MW; 98F93070C4901AAB CRC64;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=29338;
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Last annotation update)
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Pred. No. 0;
0; Mismatches
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
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                                                                                              LIDOKITDSVRKTALAGLOGLGDGLDVYQKSLKNWLRNRNDTRARSVVVTQYIALELDFV
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                                                                                                                                                                                                                                                                                                                                                             42.1%; Score 2545.5; DB 2; Length 1228; larity 43.8%; Pred. No. 1.6e-136; Conservative 183; Mismatches 381; Indels 151;
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InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PP00555; endotoxin; 1.
Pfam; PP03944; endotoxin C; 1.
Pfam; PP03945; endotoxin N; 1.
SEQUENCE 1228 AA; 139521 MW; 3DA2A4DBF59C95C3 CRC64;
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558; Conserv
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                                    LKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLPVTISGTRIYSINVNKTMNKGD
            NASSPARYGNLPVPANTHRSADVTNTVYSDKITQIPVVKAHTLVSGTTVIKGPGPTGGNI
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"Characterization of crylB gene and its flanking regions cloned from
"Characterization of crylB gene and its flanking regions cloned from
Bacillus thuringiensis subsp. entomocidus HD-9.";

Bubmitted (MAR-2001) to the BMBL/GenBank/DDBJ databases.

EMBL; AF363025; AAK51084.1; -.

GO; GO:0015070; F:toxin activity; IEA.

GO; GO:0006952; P:defense response; IEA.

InterPro; IPR001179; Endotoxin.

InterPro; IPR005638; endotoxin.
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Bacillus thuringiensis (subsp. entomocidus).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
NCBI_TaxID=1436;
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NAMPLFAIRNQEVPLLMYYAQAANLHLLLLRDASLFGSBFGLTSQBIQRYYERQVERTRD 221
                   866 ALENNGENG-NMSSDSHAPSPHIDTGEIDLNENTGIWVVPKIPTTNGYATLGNLELVERG
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                                                                                                             WNATSDVNVQQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDG 1104
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                       PLSGETLERAQQQEQQWQDKMARKRGASEKAYYAAKQAIDRLFADYQDQKLMSGVEMSDM 984
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CRYLBA.
Bacillus thuringiensis.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1428;
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1216 FIVDSVELLEMBE 1228
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1213 GETEGKFIVDSVELLIMBE 1231
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                                                                                                                                                                                                                                                                                       tch 40.3%; Score 2433; DB 2; Length 1231; al Similarity 41.8%; Pred. No. 4.3e-130; 534; Conservative 205; Mismatches 380; Indels 160;
                                                                                                                                                                                       Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                               01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
                                                                  PRELIMINARY;
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975 LANSGVEMSDMLAAQNLVQSIPYVYNDALPEIPGMNYTSFTELTNRLQQAWNLYDLRNAIP 1034
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                                                                                                        800 LLKPYTRYKLKGFIGSSODLEIKLIRHRANQIVKNVP--DNLLPDVL--PVNSCGGIDRC
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                       YRARIRYASTTNIRLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSD
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SEQUENCE FROM N.A.
Meza-Basso L.A., Theoduloz C.;
Meza-Basso L.A., Theoduloz C.;
"Cloning and expression of a delta endotoxin gene from a Chilean native Bacillus thuringiensis strain.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U94191; AAG16877.1; -.
PIR; A.29125; A.29125.
HSSP; P02965; ICIY.
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
MCBI_TaxID=1428,
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Last sequence update)
Last annotation update)
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GO, GO:0015070; F:toxin activity; IEA. GO; GO:0006552; F:defense response; IEA. InterPro; IPR001178; Endotoxin. InterPro; IPR005638; endotoxin_C.
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HSSP; P02965; 1CIY.
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GO; GO:0015070; P:toxin activity; IEA.
GO; GO:006952; P:defense response; IEA.
InterPro: IPR00178; Endotoxin.
InterPro: IPR001539; endotoxin.C.
InterPro: IPR005639; endotoxin.N.
InterPro: IPR008679; Gal bind_like.
Pfam; PP00365; endotoxin; 1.
Pfam; PP03944; endotoxin; 1.
Pfam; PP03945; endotoxin N; 1.
SEQUENCE 1155 AA; 130557 MW; 5D69E3E2P527749D CRC64;
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                                                                                        LVEEGPLSGETLERAQQQEQQWQDXMARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGV
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SPECIES=B.thuringiensis (subsp. sotto);
Zhong B.thuringiensis (subsp. sotto);
Zhong W.F., Cai P.Z., Yan W.Z., Zhang Z.X., Xiang Y.W.;
"A crylA gene cloned from Bacillus thuringiensis serovar is
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB026261; BAA77713.1; --
EMBL; APS10713; AAM44305.1; --
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
BtT84A1 crystal protein (Crystal protein CrylA).
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Bacillus thuringlensis, and
Bacillus thuringlensis (subsp. sotto).
Bacieria; Firmicutes; Bacillales; Bacillaceae;
NCBI_TaxID=1428, 29340;
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SPECIES=B.thuringiensis; STRAIN=T84Al;
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SPBCIBS=B.thuringiensis; STRAIN=T84A1;
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64 IWGIFGBSQ----WDAFLVQIEQLINQRIEBFARNQAISRLEGLSNLYQIYAESFREWEA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 AEWGPTPGEISTFYDRQVTRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLL 277
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                                                                                        : | | ; | ; | | ; | GAYESNSSVPADYASAYEKAYTDGRRDNPCESNRGYGDYTPLPAGYVTKELEYPPETDK
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ARLGNI.BFLEBKPLVGBALARVKRABKKWRDKRBKLBWBTNI VYKBAKBSVDALFVNSQY
                                                                           1033 IPNGDFRNGLSDWNATSDVNV-QQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARK
                                                                                                                                           53 NPRL-----PGNPRT-PISSSTVOTG---IGI---VGQVLGALGVPPAGQIASFYSP
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                          QKLNSGVEMSDMLAAQNIVQSIPYVYNDALPBIPGMNYTSFTELTNRLQQAWNLYDLRNA
                                                                                                                            BGVGDGYVIIRDGANQTETLTFN------ICDDDTGV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 33.9%; Score 2048; DB 2; Length 1176; al Similarity 39.3%; Pred. No. 3.8e-108; 480; Conservative 174; Mismatches 414; Indels 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=1y30;
Yao J., Zhang J., Song F., Chen Z., Li C., Huang D.;
Yao J., Zhang J., Song F., Chen E., Li C., Huang D.;
"A novel crylda gene from Bt strain ly30.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF384211; AAP80146.1;
SEQUENCE 1176 AA; 133169 WW; 725C14EA940B869B CRC64;
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Last annotation update)
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Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae;
WCBI_TaxID=1428;
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01-OCT-2003 (TrEME
01-OCT-2003 (TrEME
Delta-endotoxin.
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                                                                                                                                                           156;
                                                                                         33.9%; Score 2050; DB 2; Length 1180; 39.3%; Pred. No. 3e-108;
                                                                                                       Best Local Similarity 39.3%; Pred. No. 3e-108;
Matches 481; Conservative 173; Mismatches 414; Indels
  InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PF0055; endotoxin; 1.
Pfam; PF03944; endotoxin.C; 1.
Pfam; PF03945; endotoxin.N; 1.
SEQUENCE 1180 AA; 133489 MW; 1199E4A6D1DCE62D CRC64;
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SEQUENCE FROM N.A.
STRAIN=FU-2-7;
Kondo S., Tamura N., Kunitate A., Hattori M., Akashi A., Ohmori I.;
Kondo S., Tamura N., Kunitate A., Hattori M., Akashi A., Ohmori I.;
"Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from Bacillus thuringiensis var. kurstaki HD-1 DNA.";
Agric. Biol. Chem. 51:455-463(1987).

SEQUENCE FROM N.A.
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MEDLINE=94289859; PubMed=7764972;
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                                                                                                                                                YTLR---APTFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRR
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Length 1176;

77 77 L -> P (IN REF. 1). 965 965 S -> P (IN REF. 1). 1176 AA; 133075 MW; AA4135849A289P85 CRC64;

-> P (IN REF. 1) -> P (IN REF. 1)

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DPTNPALREEMRIQFNDWNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSVFG 179
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                                             Gaps
                                          Indels 152;
Query Match 33.8%; Score 2045; DB 2; Best Local Similarity 39.3%; Pred. No. 5.7e-108; Matches 479; Conservative 174; Mismatches 415;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=1428; [1]

(TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 25, Last annotation update)

01-NOV-1996 (TrEMBLrel. 01, Le 01-OCT-2003 (TrEMBLrel. 25, Le 10-OCT-2003 (TrEMBLrel 25, Le CRYIA(A).

CRYIA(A).

Bacillus thuringiensis.

PRT; 1176

PRELIMINARY;

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                                   SGSFRTVGFTTPFNFSNGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAEYDLERAQK
                                                                                      LLQDTGPNRING--ENGWTGSTGIEVAEGDVLFXDRSLRLTSARRIDTETYPTYLYQQID
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FNTFDLATIGTAFTFSNYSDSLTVGADSPASGGEVYVDKFELI PVNATFEAEEDLDVAKK
                                                                        AVNGLPTSKKD-ALQTSVTDYQVNQAANLVECLSDELYPNEKRMLWDAVKEAKRLVQARN
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Hou B.K., Chen 2.H.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF154676; AAD55382.1;
HSSP; P02965; 1CIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 kDa insecticidal protein.
Bacillus thuringiensis (subsp. kurstaki).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GO; GO:0006952; P:defense response; IEA.
InterPro; IPR001178; Endotoxin.C.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR008639; endotoxin.N.
InterPro; IPR008679; Gal.bind_like.
Pfam; PF00555; endotoxin.1.
Pfam; PF00344; endotoxin.C; I.
Pfam; PF03445; endotoxin.N; I.
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1157 IGETEGTPIVDSVELLIMEB 1176
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973 OKLNSGVEMSDMLAAQNLVQSIPYVYNDALPEIPGANYTSFTELTNRLQQAWNLYDLRNA 1032
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                                                                                                                                                                                                                                                                                                                        277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLQDTGFNRING--ENGWTGSTGIEVAEGDVLFKDRSLRLTSAREIDTETYPTYLYQQID 797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 NPEL------PGNPET-PISSSTVQTG---IGI----VGQVLGALGVPPAGQIASFYSP
                                                                                                                                                                             98 IVGQLWPSSTVSVWEMIMKQVEDLIDQKITDSVRKTALAGLGGLGDGLDVYQKSLKNWLB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSGSVGGFTYSKPHTTMQVCTQNYNTIDRIPPBNB--PLSRGYSHRLSHITSYSFSKNAS
                                                                                                                            4 NPNINECIPYNCLSNPEVEVLGGGRIBTGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDI
                                                                                                                                                                                                                                                                                                                          218 AEWGFTPGEISTFYDROVTRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREWTLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501 SPARYGNLPVFAWTHRSADVTWTVYSDKITQIPVVKAHTLVSGTTVIKGPGFTGGNILKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445 YTLR---APTFSWQHRSABFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     621 FNTFDLATIGTAFTFSNYSDSLTVGADSPASGGEVYVDKFELIPVNATFRABBDLDVAKK
                                                                     Gaps
                                Ouery Match 33.7%; Score 2034; DB 2; Length 1176; Best Local Similarity 39.2%; Pred. No. 2.4e-107; Matches 478; Conservative 173; Mismatches 417; Indels 152;
1176 AA; 133010 MW; PCEE069D0B81D8C4 CRC64;
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SEQUENCE
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980 EMSDMLAAQNLVQSIPYVYNDALPEIPGMNYTSPTELTNRLQQAWNLYDLRNAIPNGDFR 1039
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                                                                                                                                                                                                                                                                                        504
                                                                                                                                                                                                                                                                                                                                 563 SGPLAYTSVSVKSPLSORYRARIRYASTTNLRLFVTISGTRIYSINVNKTMNKGDDLTFN 622
                                                                                                                                                                                                                                                                                                                                                           447 VGGPTYSKPHTTMQVCTQNYNTIDEIPPENB--PLSRGYSHRLSHITSY--SFSKNASSP
                                                                                                                                                                                       LPSAVYRKSGTV-----DSLDEIPPQNNNVPPRQGPSHRLSHVSMPRSGFSNSSVSI
                                                                                                                                                                                                                                                                                                                                                                                                                   623 TFDLATIGTAFTPSNYSDSLTVGADSPASGGEVYVDKFELIPVNATFEAEBDLDVAKKAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ODPNPRGINROLDRGWRGSTDITIQGGDDVPKRNYVTLLGTFD---ECYPTYLYQKIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     800 LLKPYTRYKLKGFIGSSODLEIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSBQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            742 KLKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETVNVPGT--GSLWPLSAPSPIGKCAHH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       960 YVDANLALENNGENGNMSSDSHAPSFHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARYGNL PVPAWTHRSADVTNTVYSDKITQI PVVKAHTLVSGTTVI KGPGFTGGNI LKRTS
                                                                                                                                                                                                                                                                       -----YITKTVBFTPSTEQVWIDMSE
AVIRSPHIPDILSEIEPYTTRAGLPLANTEYLEYWYGHSIK-----YKNTNASSALERNY
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Last sequence update)
Last annotation update)
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(TrEMBLrel. 04,
(TrEMBLrel. 25,
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1118
                                                                                                                                                               DTGVLSADQTS-----YITKTVEFTPSTEQVWID 1147
                                                                                                                                                                                         : : || | ::|||;
EAPSVPADYASVYEEKSYTDGRRENPCEFNRGYRDYTPLPVGYVTKELEYFPETDKVWIE 1156
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Yu J., Tan L., Wu D., Pang Y.;
"Molecular characterization of a silent gene encoding a 130-kilodalton crystal protein from Bacillus thuringtensis subap. israelensis.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF375608; AAK55546.1;
                                                                                                         4 NPNINECI PYNCLSNPEVBYGGERIETGYTPIDISLSLYQFLLSEFVPGAGFVLGLVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRNDTRARSVVVTQYIALELDFVAKIPSFAISGOBVPLLSVYAQAANLHLLLLRDASIFG
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                                                                                 EGVGDGYVIIRDGANQTETLTFN------ICDD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 33.6%; Score 2032.5; DB 2; Length 1155; Best Local Similarity 38.9%; Pred. No. 2.9e-107; Matches 473; Conservative 185; Mismatches 392; Indels 167;
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GO; GO:0006952; P:defense response; IEA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PP00355; endotoxin; 1.
Pfam; PP03944; endotoxin; 1.
Pfam; PP03944; endotoxin; 1.
Pfam; PP03945; endotoxin; 1.
SEQUENCE 1155 AA; 130747 MW; 7F0C98E0100C7698 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                   1148 MSETEGVPNIESVELVLEER 1167
                                                                                                                                                                                                                                                                           Crystal protein CrylAbl6.
CRY1AB16.
Bacillus thuringiensis (s
                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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093121
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DT 01-DB
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                                                                                          -GENGWICSTGIEVARGDVLFKDRSLRLISAREIDTETYPTYLYQQIDESLLKPYTRYKL
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508 INSPITORYRLRFRYASSRDARITVAIGGOIRVDMTLEKTMEIGESLTSRTFSYTNFSNP
                                                             PTFSNYSDSLTVGADSPASGGEVYVDKFBLIPVNATFRAEBDLDVAKKAVNGLFTSKKD-
                                                                                                                                                                                 692 ALQTSVTDYQVNQAANLVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRIN-
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SITAIN-B-Pr-88;

C. STRAIN-B-Pr-88;

A. Li G., Zhang J., Li G., Huang D.;

I. C., Zhang J., Li G., Huang D.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

R. EMBL; AF288683; AAO13756.1;

EMBL; AF288683; AAO13756.1;

R. GO; GO:0006952; P:defense response; IRA.

R. InterPro; IPR001178; Endotoxin.

R. InterPro; IPR005639; endotoxin.

R. InterPro; IPR005639; endotoxin.

R. InterPro; IPR005639; endotoxin.

R. InterPro; IPR00555; endotoxin.

R. Pfam; PF00555; endotoxin.
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1428,
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Barboza-Corona J.B., Lopez-Meza J.B., Ibarra J.B.;

"Cloning and expression of the crylEa4 gene of Bacillus thuringiensis and the comparative toxicity of its gene product.";

World J. Microbiol. Biotechnol. 14:437-441(1998).
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Pfam; PF03944; endotoxin_C; 1.
Pfam; PF03945; endotoxin_N; 1.
SEQUENCE 1171 AA; 133310 MW; 333603A1A782523A CRC64;
                                                             Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=LBIT-147;
Ibara J.E., Barboz-Corona J.E.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U94323; AAD04732.1; -.
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HSSP; P02965; ICIY.
GO; GO:0015070; P:toxin activity; IEA.
GO; GO:000592; P:defense response; IEA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008639; endotoxin.N.
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EMBL; AF215647; AAF37224.1; -.

EMBL; AF215670; F:toxin activity; IRA.

GO; GO:0015070; F:toxin activity; IRA.

GO; GO:0015070; F:toxin activity; IRA.

InterPro; IPR00178; Endetoxin.C.

InterPro; IPR00178; Endetoxin.C.

InterPro; IPR005638; endetoxin.C.

R InterPro; IPR008639; endetoxin.C.

R Pfam; PF00555; endetoxin; 1.

Pfam; PF00555; endetoxin; 1.

Pfam; PF00555; endetoxin.C; 1.

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Last annotation update)
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                                                                                                                                                                                                  1138 TPSTEQVWIDMSETEGVFNIESVELVLEEE 1167
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Bacillus thuringiensis.
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                                                                                                                                                                                                                                                   EMTLLVLDLVALPPNYDTRTYPIETTAQLTREVYTDPIVFNRETSGGFCRRWSLNSDISF 332
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                                                                                                   Gaps
                                                                                                   148;
                                                             Length 1169;
                                                                                                 Indels
Pfam; PF01945; endotoxin_N; 1.
SEQUENCE 1169 AA; 132990 MW; 07C9D6D180F3DB6D CRC64;
                                                           Query Match
33.1%; Score 2003; DB 2; Best Local Similarity 39.3%; Pred. No. 1.4e-105; Matches 460; Conservative 173; Mismatches 389;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
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                                                                                                             SEQUENCE PROM N.A.
                                                                                                                                                STRAIN=BTS00349A;
                                                                                                                                                                                                      "NO INFORMATION."
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                                                                                IPQVRSLGADLANYYAQVYGVPYASFTLLLDRNTGSGSVGGFTYSKPHTTMQVCTQNYNTI 469
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59 NPRTPISSSTVQTG-----IGIVGQVLGALGVPPAGQIASPYSFIVGQLWPSSTVSVW 111
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UN 121

P. SEQUENCE PROM N.A.

C. STRAIN=B-Pr-88;

A. Li C., Zhang J., Huang D., Li G.;

Lu C., Zhang J., Huang D., Li G.;

Lu Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

S. Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

P. Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

P. Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

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P. R. Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

P. R. Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

P. R. Submitted (JAN-2001) to the EMBL/GenBank/DDBJ GASSONS INT.

P. Submitted (JAN-2001) to the EMBL/GenBank/DDBJ emdotoxin N.

P. R. InterPro; IPRO0595; endotoxin J.

D. P. Fam; PRO0595; endotoxin N; 1.

P. Fam; PRO0595; endotoxin N; 1.

S. SEQUENCE 1174 AA; 133350 MM; 8C7F122P9446F15C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 YIALELDFVAKIPSFAISGOEVPLLSVYAQAANLHLLLLKDASIFGAEWGFTPGEISTFY
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1053 V-QQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETL 1111
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YQVNQAANLVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRIN--GENGWTG 757
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                                                                         STGIEVAEGDVLFKORSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGPIGSSQ 817
                                                                                 818 DLEIKLIRHRANQIVKNVP--DNLLPDVL--PVNSCGGIDRCSEQQYVDANLALENNGEN 873
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Copyright (c) 1993 - 2004 Compugen Ltd.
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1 MSPNNQNEYBILDASSSTSV.......MSBTEGVFNIESVBLVLEEB 1167 US-10-089-678-1 score: Sequence: Title: Perfect :

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched: 1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp20028:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:* A Geneseq 29Jan04:* geneseqp2000s:* geneseqp2001s:* geneseqp1980s:* geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STEMMARTES

	Description	Aau80281 Bacillus	Aar28900 Toxin 50C		Aar33768 Bt isolat	-			_			ın	_ `	Aaw84581 Amino aci	Amino		_	Aaw84575 Amino aci		•		Aaw84588 Amino aci		Aaw84576 Amino aci	Aar48678 Insectici	Aaw84570 Amino aci
SUPMARIES	A	AAU80281	AAR28900	AAR25997	AAR33768	AAW06418	AAR27343	AAR44208	AAR32354	AAR51692	AAU99256	AAU99255	AAW06417	AAW84581	AAW84584	AAW84571	AAW84591	AAW84575	AAW84586	AAW84582	AAW84593	AAW84588	AAW84578	AAW84576	AAR48678	AAW84570
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Aaw84566 Amino aci Aaw84569 Amino aci Aaw84568 Amino aci Aaba2178 Cruor H1	Amino Amino Amino	Amino Amino Amino		Aaw44580 Amino aci Aaw44574 Amino aci Aaw46857 Bacillus Aay24960 Bacillus Aau02034 B. thurin
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25 26 28 28	38888	4 6 6	37 38 40	4 4 4 4 1 4 4 4 4 1 4 4 4 6

ALIGNMENTS

Bacillus thuringiensis insecticidal protein. Insecticide; transgenic; Coleoptera larvae. AAU80281 standard; protein; 1167 AA. 03-AUG-2000; 2000JP-00236140. 03-AUG-2000; 2000JP-00236140. 30-JUL-2002 (first entry) Bacillus thuringiensis. JP2002045186-A. 12-PEB-2002

(SDSB-) SDS BIOTECH CORP.

WPI; 2002-356468/39.

A protein having insecticidal activity, a DNA encoding said protein, and an agent and a method for preventing harmful organisms.

Claim 1; Page 9-12; 19pp; Japanese.

This invention relates to a crystalline protein comprising a fully defined sequence and the mucleotide sequence encoding this protein. The protein of the invention is an agent for preventing barmful organisms comprising Bacillus thuringlensis serovar galleriae SDS502, its mutant or a microbe transformed by a DNA encoding the protein. This microbe can be used to produce a protein containing the protein, or containing a protein having insecticidal activity produced by the SDS502, its mutant or a transformed microbe, a microbe which is transformed by using the above or a seed transformed by using the above DNA, and producing a protein or a seed transformed by using the above DNA, and Bacillus thuringiensis serovar galleriae SDS502 producing a protein comprising and producing a protein showing insecticidal activity. The protein of the invention may have insecticidal activity. The agent is used for preventing Coleoptera larvee. This sequence represents the Bacillus thuringiensis insecticide protein of the invention

Sequence 1167 AA;

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Payne JM, Cannon RJC,
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30-SEP-1991;
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                                             MSPNNQNBYE1LDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
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                                                                                                                      LIDOKI TDSVRKTALAGLOGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 BTPISSSTVQTGIGIVGQVLGALGVPPAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVED 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endotoxin; acarides; pest; Two Spotted Spider;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus thuringiensis; kumamotoensis PS50C
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27-JAN-1993
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                                                                                                                                 181 AKIPSFAISGQEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQVTRTAQ 240
                                                                                                                                                                                                            YSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLLVLDLVALPPNYDTRTYPIETTAQ 300
                                                                                                                                                                                                                                  YSDYCVKWYKIGLDKLKGTTSKSWLNYHQFRREMTLLVLDLVALFPNYDTHWYFIETTAQ 300
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The sequence given is an approx. 130 kD protien known as Bacillus thuringiensis PS50C (B.t.PS50C). This novel delta-endotoxin has been shown to be active against the Colorado potato beetle (Leptinotarsa decemlineata). The gene encoding this toxin can be transformed into suitable hosts such as Pseudomonas, which can then be applied to the environment of coleopteran insects where they will proliferate and be ingested by the insects. This DNA sequence can be inserted into an expression vector which contains a promoter/operator region, a ribosome binding site, polyadenylation signals, etc. This will allow transcription and translation of the cells in the appropriate host. (Updated on 25-MAR-2003 to correct PN field.)
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1129 PYTDOMWIEISETEGTFYIESVELIVDVE 1157
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KA, Bradfish GA

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Controlling lepidopteran pests - using compsn. of Bacillus strains or plants or microorganisms transformed with their
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                                                        Bacillus thuringiensis
                                     Lepidopteran-active;
                                                                                                                                                               (MYCO ) MYCOGEN CORP.
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15-JUL-1993 (first
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08-SEP-1992;
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                                                           YLGDTIEKARFUKTMDNGASLTYETFKFASFITDFOFRETODKILLSMGDFSGGGEVYID
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                                                LTREVYTOPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSEIBPYTTRAG
                                                                                     LPLNNTEYLEYWYGHSIKYRNT-NASSALERNYGTITSNKIKYYDLANKDIFQVRSLGAD
                                                                                                LANYYAQVYGVPYASPTLLDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTIDEIPPENE-P
                                                                                                                                                                 LSRGYSHRLSHITSYSPSKNASSPARYGNLPVPANTHRSADVTNTVYSDKITQIPVVKAH
                                                                                                                                                                                                      TLVSGTTVIKGPGPTGGNILKRISSGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLPVT
                                                                                                                                                                                                                       MLYLGGSVVQGPGPTGGDILKRTNPSILGTPAVTVNGSLSQRYRVRIRYASTTDFB-FTL
                                                                                                                                                                                                                                           599 ISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGEVYVD
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thuringiensis toxin genes.

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The sequences given in AAR33768-70 represent lepidopteran-active toxins. The DNA encoding these sequences were used within a Ti or Ri plasmid, to transform plant cells. Whole plants can then be regenerated from the transformed cells. The toxin may also be produced by cloning Bacillus thuringiensis (Bt) . It may then be applied directly to the plant locus. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                          ETFISSSTVQTGIGIVGQVLGALGVPPAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVED
                                                                                                                                                                                                                                                                                                                                                           RTF1SSST1QTG1UGR1LGALGVPPASQ1ASPYSP1VGQLWPSKSVD1WGB1MBRVEE
                                                                                                                                                                                                                                                                                                                                                                                                                AKI PSPAISGOEVPLISVYAQAANI.HILILIRDASI PGAEWGPTPGEISTPYDRQVTRTAQ
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                                                                                                                                                                                                                                                        MSPNNONBYBILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSBGENPBLFGNP
                                                                                                                                                                                                                                                                                                                                                                                              LIDOKI TDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQY IALBLDPV
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                                                                                                                                                                                                                         Gape
                                                                                                                                                                                                                     14;
                                                                                                                                                                                      Length 1157;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                   Match 66.3%; Score 4007; DB 2; Local Similarity 66.1%; Pred. No. 1.9e-255; Les 773; Conservative 144; Mismatches 238;
                                                                                                                                                    Sequence 1157 AA;
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protein; 1157

standard;

AAR33768

AAR33768

AAR33768

(revised)

25-MAR-2003

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RLOQAMMLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIPNWNSQVSQQFTVQ 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPBIPGMNYTSFTELTN 1018
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LANYYOKAYGVPGSWFHMVKR--GTSSTTAYLYSKTHTALOGCTQVYBSSDBIPLDRTVP 477
                                                                                                                              YLGDTIEKNRFNKTMDNGASLITYETFKFASFITDFQPRETQDKILLSNGDFSSGQEVYID
                                SE STARTSHITSHSFSKNGS--AYYGSPDVFVWTHTSADLANTIYSDKITQIPAVKGD
                                                                                                                                                               KPELI PVNATFEAEEDLDVAKKAVNGLFTSKKDALQTSVTDYQVNQAANLVECLSDELYP
                                                                                                                                                                           TLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLFVT
                                                                                                               ISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGEVYVD
                       LSRGYSHRLSH1TSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVYSDK1TQ1PVVKAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSTEQUWIDMSETEGVFNIESVELVLEEB 1167
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PYTDQMWIBISETEGTPYIBSVBLIVDVB 1157
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Toxin 50C(a); scarab pest; toxin; insect; scarabaeidae; pest control; larval stage insect; grain; tuberous crop; white grub; chafer grub; cyclocephala; popillia.
                                                                                                                                              sacillus thuringiensis; strain kumamotoensis
                  Ź
                 AAW06418 standard; protein; 1157
                                                                                    Antiscarab pest toxin 50C(a)
                                                       (revised)
(first entry)
                                                       16-OCT-2003
28-JAN-1997
                                                                                                                                                                                       10-SEP-1996
                                     AAW06418;
       RESULT
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300

180

120

9 9 120

360 419 419 LANYYAQVYGVPYASFTILIDKATGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPPENB-P 478

LPLANTEYLEYWVGHSIKYKNT-NASSALERNYGTITSNKIKYYDLANKDIFQVRSLGAD

361 361 420

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420

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94US-0031546B

30-SEP-1994;

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The DNA encoding this sequence was isolated from the Bacillus
The DNA encoding this sequence was isolated from the Bacillus
The DNA encoding this sequence was isolated from the Bacillus
Thuringiensis strain kumamoteensis. Insects in the family Scarabaeidae
constitute a serious pest control problem, especially when destructive
larval stage insects infest high value turf found in golf courses.

The larvae are known as white grubs, or chafter grubs, and ornamentals. The larvae are known as white grubs, or chafter grubs, and cnameentals. The larvae and the U.S. populations of where they consume plant roots. In Burope and the U.S. populations of these larvae and adults have developed resistance to chemical
insecticides such as the organochlorines and DDT. These toxin sequences, and intact calls that are capable of expressing these proteins, can be used to control many peets of the family scarabaeidae, such as species of Cyclocephala, and Popillia. The toxins are active against larvae (present in soil) and against adults. (Updated on 16-OCT-2003 to standardise OS
field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 YSDYCVKWYKIGLDKLKGTTSKSWLNYHQPRREMTLLVLDLVALPPNYDTHMYPLRTTAQ 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 LIDOKITDSVRKTALAGIOGIGDGLDVYOKSLKWIENRNDTRARSVVVTQYIALBLDFV 180
                                                                                                                                                                                                        New nucleic acid encoding B.thuringiensis toxin active against scarab(s) - also related toxin and transformed microbes, effective against adult pests and their larvae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETPISSSTVQTGIGIVGQVLGALGVPPAGQIASPYSPIVGQLWPSSTVSVWEMIMKQVBD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AKIPSPAISGQEVPLLSVYAQAANLHLLLLRDASIFGAEWGPTPGBISTFYDRQVTRTAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 66.3%; Score 4007; DB 2; Length 1157; Local Similarity 66.1%; Pred. No. 1.9e-255; Length 144; Mismatches 238; Indels 14
                                                                                                                     Michaels TE;
                                                                                                                                                                                                                                                                                     Example 2; Col 21-26; 24pp; English.
              91US-00808316.
92US-00828430.
93US-00014941.
                                                                                                                       Narva KB,
                                                                                    (MYCO ) MYCOGEN CORP
                                                                                                                                                         WPI; 1996-424659/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1157 AA;
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                                                                                                                       Foncerrada L,
              16-DEC-1991;
30-JAN-1992;
01-PEB-1993;
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                                                                                                                                                                 SESYSHRISHITSHSFSKNGS--AYYGSFPVFVWTHTSADLANTIYSDKITQIPAVKGD
                                                                         YLGDTIEKNRENKTWENGASLTYETFKFRASFITDFQFRETQDKILLSMGDFSSGQEVYID
                                                                                                          RIEFIPVDETYBARQDLEAAKKAVNALFTNTKDGLRPGVTDYEVNQAANLVBCLSDDLYP
                                                                                                                                  NEKRMI, WDAVKEAKRLVQARNII, QDTGFNR INGENGTGSTGIEVAEGDVI, PKDRSIRLT
                                                                                                                                            LLPDVSPVNSDGSINRCSEOKYVNSRL-----EGENRSGDAHEFSLPIDIGELDYNENA
                                                                                                                                                                                                                                               AKQAIDRLPADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPBIPGMNYTSFTBLTN
                                                                                                                                                                                                                                                                                                                RLQQAWNLYDQRNAIPNGDFRNGLSNWNATPGVEVQQINHTSVLVIPNWDEQVSQQFTVQ
LSRGYSHRLSHITSYSFSKNASSPARYGNLPVPAWTHRSADVTNTVYSDKITQIPVVKAH
                                TLVSGTTVIKGPGFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLFVT
                                         MLYLGGSVVQGPGFTGGDILKRTNPSILGTFAVTVNGSLSQRYRVRIRYASTTDFR-FTL
                                                                 599 ISGTRIYSINVNKTMNKGDDLFFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGBVYVD
                                                                                                  KPEL I PVNATPRAREDLDVAKKAVNGLPTSKKDALQTSVTOYQVNQAANLVRCLSDELYP
                                                                                                                                                                                                    LLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMSSDSHAPSFHIDTGEIDLNENT
                                                                                                                                                                                                                                     GIWWYFKI PTTNGYATLGNLBLVEEGPLSGETLERAQQQEQQWQDKWARKGASEKAYYA
                                                                                                                                                                                                                                                                                                       RLOQAWNLYDLRNA! PNGDFRNGLSDWNATSDVNVQQLSDTSVLVI PNWNSQVSQQFTVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beetle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B-18746; pMYC1638; Colorado potato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B.thuringiensis PS50C Coleopteran-active toxin.
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PYTDQMWIEISBTEGTFYIBSVELIVDVB
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92US-00812180.
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02-JAN-1992;
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                                                                                                    The toxin can be used to control coleopteran pests, esp. soil-inhabiting coleoptera. The C-terminal Glu residue corresponds to a CAG (Gln) codon. The protein is obtained from a new isolate of Bacillus thuriengiensis
                                      and
                                                                                                                                                                                                                                                                                                   SSIPSPAVSGHEVILLAVYAQAVNLHILILLRDASIPGBEWGFTPGBISRFYNRQVQLTAB
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                                      New Bacillus thuringiensis isolate - used for preparing to transformed hosts for controlling coleoptera insect pests
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66.1%; Score 3995; DB 2;
Best Local Similarity 66.0%; Pred. No. 1.2e-254;
Matches 771; Conservative 145; Mismatches 239;
                                                                                Claim 12; Page 18-20; 33pp; English
1992-323784/40
                                                                                                                                                                Sequence 1157 AA;
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                                           Match 66.1%; Score 3994; DB 2; Local Similarity 66.0%; Pred. No. 1.4e-254; es 771; Conservative 144; Mismatches 240;
correct PF field.)
                       Sequence 1157 AA;
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GIWVGFKITDPEGYATLGNLELVEEGPLSGDALERLQREEQQWKIQWTRRREFIDRRYMT
                                                                                                                                                                                 RLOQAMNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI PNWNSQVSQQFTVQ
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                                            LLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMSSDSHAPSFHIDTGEIDLMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spider mite - utilising
into microbe hosts.
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biological control agent; transgenic plant; crop improvement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The protein sequence is that of a toxin active against Coleoptera that is produced from a pure culture of Bacillus thuringiensis serovar japomesis variety Buibui (FERM BP-3465). The toxin is a delta-endotoxin which has a mol. wt. of ca. 130 kD. It is useful for control of coleoptera larvae e.g. it is effective against Anomala cuprea but has little effect on Lepidoptera. The toxin can be used as B.t. spores or crystals, as opt. treated cells (B.t. or transformed microorganisms) or it is expressed by plants. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain of Bacillus thuringiensis serovar japonensis - producing toxin
PNORYVIRVTARKEGVGVGYVSIRDGGNQSETLIFSASDYDTNGVYNDQTGYITKTVTFI
                                                        RLQQAWNLYDLRNAI PNGDFRNGLSDWNATSDVNVQQLSDTSVLVI PNWNSQVSQQFTVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           crystal; Bacillue;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delta-endotoxin; larvae; Anomala cuprea; spore;
thuringiensis; virus; insect; FBRM BP-3465.
                                                                                                                                                                                                                            PSTEQVWIDMSETEGVPNIESVELVLEEE 1167
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                                                                                                                 QLTREVYTOPIVFNRETSGSPCRRWSLN----SDI-----SPSEVESAVIRSPHLPDIL
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301 KLTREIFTDPV------GSYVTGQSSTLISWYDMIPAALPSFSTLEN-LLEKKDPFTLL
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301 BLTREIFTDPV-----GSYVTGQSSTLISWYDMIPAALPSFSTLEN-LLEKKPDFFTLL
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             241 RYSDHCVQWYNAGLNKURGTGAKQWUDYNRFRREMNVMVLDLVALFPNYDARIYPLETNA
                                                  300 QLTREVYTDPIVFNRETSGGPCRRWSLN----SDI-----SFSEVESAVIRSPHLFDIL
                                                                                                                                                                      867 GAMSSDSHAFSFHIDTGEIDLAENTGIMIVFKIPTTWGNATLGALEFVBBGPLSGBTLEW
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240 QYSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLLVLDLVALPPNYDTRTYPIBTTA
                                                                                                                                                      DIFOVRSLGADLANYYAQVYGVPYASPTLLDKWTGSGSVGGPTYSKPHTTMQVCTQNYNT
                                                                                                                                                                                                                                                          526 SDKITOIPVVKAHTLVSGTTVIKGPG-PTGGNILKRISSGPLAY---ISVSVKSPLSORY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This insecticidal protein has activity against Coleopteran insect larvae and has been isolated from Bacillus thuringiensis serovar japonensis strain Buibui. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSPNNQNBYEIIDALSPTSVSDNSIRYPLANDQTNTLQNMNYKDYLAMTBSTNABLSRNP
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751. .766
/note= "amino acids 751-766 are not given in the
specification and so have been decoded from AAQS8975"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA from Bacillus thuringiensis serovar - useful in insecticides against Coleoptera
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                         B.thuringiensis serovar Japonensis insecticidal
                                                                                                                                                                                                                                   insecticidal protein; Coleoptera larvae; Buibui
                                                                                                                                                                                                                                                            Bacillus thuringiensis; (serovar Japonensis strain Buibui).
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                                                                                                                   AAR51692 standard; protein; 1149
                                                                                                                                                                                                                                                                                                                                                                                                                      92JP-00213886
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                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insecticidal protein and Japonensis strain Buibui
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N-PSDB; AAQS8975.
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04-NOV-1994
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                                                                                                                                                                                                                                                                                                                     The present invention relates to a new pesticidal polypeptide. The invention is useful for impacting an insect pest by applying the the molecules of the invention to the environment of the insect pest by spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn rootworm or southern corn rootworm. The invention is also useful for increasing insect target range and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also useful for producing transformed plants and in transforming any organism to produce the pesticidal polypeptide of the invention. The present amino acid sequence represents a Bacillus thuringiensis wild-type Cry1218
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                Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest
Colorado potato beetle; western corn rootworm; southern corn rootworm;
insect target range; endotoxin; Cry1218.
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Sacillus thuringiensis Cry1218-2 protein sequence.
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23-OCT-2001; 2001US-00032717.
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                                                     ------EIPPE--NEPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVPAWTHRS
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  415 VLLDIVYPGYTYIFFGMPEVEFFWVNQLNNTRK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a new pesticidal polypeptide. The invention is useful for impacting an insect pest by applying the the molecules of the invention to the environment of the insect pest by spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn rootworm or southern corn rootworm. The invention is also useful for increasing insect target range and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also useful for producing transformed plants and in transforming any organism to produce the pesticidal polypeptide of the invention. The present amino acid sequence represents a Bacillus thuringiensis wiid-type Cry1218 endotoxin protein
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                                                                                                                                                                                   24-OCT-2001; 2001WO-US045468
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23-OCT-2001; 2001US-00032717.
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                                                                                                                                                                                                                                                                     AAW06417-W06419 represent toxins that are active against scarab pests.

The DNA encoding this sequence was isolated from the Bacillus thuringiensis strain kumanotoensis. Insects in the family Scarabaeidae constitute a serious pest control problem, especially when destructive larval stage insects infest high value turf found in golf courses, is playing fields and lawns. The larvae of many species also attack grains, tuberous crops, and ornamentals. The larvae are known as white grubs, or chafer grubs, and can be found in decaying organic matter, or in the soil where they consume plant roots. In Burope and the U.S. populations of these larvae and adults have developed resistance to chemical insecticides such as the organochlorines and DDT. These toxin sequences, and intact cells that are capable of expressing these proteins, can be used to control many pests of the family scarabaeidae, such as species of Cyclocephala, and Popillia. The toxins are active against larvae (present in soil) and against adults. (Updated on 16-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTPIS-SSTVQTGIGIVGQVLGALGVPFAGQIASPYSFIVGQLWPSSTVSVWEMIMKQVB 119
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                                                                                                                                                                                            New nucleic acid encoding B.thuringiensis toxin active against scarab(s) - also related toxin and transformed microbes, effective against adult pests and their larvae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSPNNQNEYEIIDATPSTSVSNDSNRYPFANEPTNALQNMDYKDYKASAGNVSEYPGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.2%; Score 3152; DB 2; Length 1169; Best Local Similarity 54.0%; Pred. No. 5.7e-199; Matches 653; Conservative 179; Mismatches 294; Indels 84;
                                                                                                                                   Michaels TE;
                                                                                                                                                                                                                                                Claim 2; Col 29-36; 24pp; English.
                                                         91US-00808316.
92US-00828430.
93US-00014941.
                                   94US-00315468
                                                                                                                                   Foncerrada L, Narva KE,
                                                                                                          (MYCO ) MYCOGEN CORP.
                                                                                                                                                             1996-424659/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1169 AA;
                                                                                                                                                                         N-PSDB; AAT43221.
                                   30-SEP-1994;
                                                          16-DEC-1991;
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01-FEB-1993;
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                                                                              DEIPPE--NEPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVYSD
                                                                                                                                                                     KI TOI PVVKAHTLVSGTTVI KGPGPFGGNI LKRTSSGPLAYTSVSVKSPLSQRYRARIRY
                                                                                                                                                                                            AS--TINLRLF-VTISGTRIYSINVNKT-MNKGD-DLTFNTFDLATIGTAFTFSNYSDSL
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Synthetic.
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PVVKAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTN

ENBPLSRGYS-HRLSHITSYSPSKN-ASSPARYGNLPVFAWTHRSADVTNTVYSDKITQI

GADLANYYAQVYGVPYASFIL -- LDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTIDBIPP

646 638 706 698 764

NLVECLSDBLYPNEKRMLMDAVKEAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVA

DSPASGGEVYVDKPRLI PVNATPRABEDLDVAKKAVNGLFTSKKDALQTSVTDYQVNQAA

814 884

RHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSBQQYVDANLALENNGENGNMSSDSHAPS

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1065 FNWNSQVSQQFTVQPNYRYVLRVFARKBGVGBGYVIIRDGANQTETLIFRICDDDTGVLS 1124
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Local Similarity 52.4%; Pred. No. 2.2e-197;
les 620; Conservative 195; Mismatches 326; Indels
                                                                                                                          (PLBZ ) PLANT GENETIC SYSTEMS NV
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                                                              98WO-EP004033
                                                                                            97US-00884389
                                                                                                                                                           Van Rie J;
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                                                              25-JUN-1998;
                                                                                            27-JUN-1997;
 WO9900407-A2
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Amino acid sequence of Bacillus thuringiensis Cry9C mutant
Cry9C; crystal protein; toxic; mutant; insecticide; transgenic plant; transgenic seed; lepidoptera.
                                                                                                AAW84584 standard; protein; 1157 AA
                                                                                                                                                      07-JUN-1999 (first entry)
                                                                                                                                                                                                                                                 Bacillus thuringiensis.
Synthetic.
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                                                                                                                           AAW84584;
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                                                                                     QYSDYCVKWYNTGLDRCKGTNAASWLKYHQPRREWTLLVLDLVALPPNYDTRTYPIETTA 299
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                 61 ETPISS-STVQTGIGIVGQVLGALGVPPAGQIASFYSPIVGQLWPSSTVSVWEMIMKQVR 119
                                                                        DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDF
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SHWDAQVSQQLRVNPNCKYVLRVTARKVGGGGGYVTIRDGAHHQRTLTFNACDYDVNGTY 1114

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1065 PNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTBTLTFNICDDDTGVLS 1124
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                      PVVXAHTLVSGTTVI KGPGFTGGNI LKRTSSGPLAYI SVSVKSPLSORYRARI RYASTTN
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                                                                                                                                                                                                                              LRLFVTISGTRIYSINVNKTMNKGDDLTFNTF---DLATIG---TAFTFSNYSDSLTVGA
417 GADLANYYAQVYGVPYASPTL--LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP
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                                                                                                                                                                                                                            New Bacillus thuringiensis Cry9C crystal proteins with improved toxicity - useful for producing transgenic plants in controlling pest insects, especially Ostrinia nubilalis, Heliothis virescens and Diatraea
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Matches 620; Conservative 195; Mismatches 326; Indels
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                                                                                                              (PLBZ ) PLANT GENETIC SYSTEMS
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                                      98WO-EP004033
                                                                          97US-00884389
                                                                                                                                                    Van Rie J;
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                                                                                                                                                                                                                                                                                      grandiosella.
                                                                        27-JUN-1997;
                                    25-JUN-1998;
07-JAN-1999
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(PLBZ ) PLANT GENETIC SYSTEMS NV.
98WO-EP004033.
     97US-00884389
               Van Rie J;
                    WPI; 1999-105666/09
25-JUN-1998;
               Roeck S,
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New Bacillus thuringiensis Cry9C crystal proteins with improved toxicity - useful for producing transgenic plants in controlling pest insects, especially Ostrinia nubilalis, Heliothis virescens and Diatraea grandiosella.

Example; Page; 40pp; English.

This is the amino acid sequence of a Cry9C (crystal) mutant protein which is toxic to an insect species. It is modified in the method of the invention in an attempt to improve its toxicity. The improved proteins are useful for producing transgenic plants and seeds in controlling are useful for producing transgenic plants and seeds in controlling insects feeding on a plant. The transgenic plants are also useful for producing more transgenic plants with similar characteristics, or for introducing the improved cry9C gene (including fragments) into the same plant variety or related plant species. The Cry9C protein can be obtained from cultured colls of the transgenic plants and used in insecticide compositions against lepidopteran insects, especially Ostrinia nubilalis, Heliothis virescens and Diatraea grandiosella. The cry9C gene can be expressed in combination with another insect control protein (e.g. Another B thuringiensis derived crystal protein, especially Cry1Ab- or Cry1B-type protein), and used to transform B thuringiensis, which crystoprotein of insect pests, or insects where insect resistance development is specification, but is generated using the information provided by the inventors.)

Sequence 1157 AA;

QXSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLLVLDLVALPPNYDTRTYPIETTA 299 GLPLNNTEYLEYWYGHSIKYKNTNASSALERNYGTITSNKIKY---YDLANKDIFQVRSL 416 - PPV-SSNFWDYWSGHTLRRSYLNDSAVQEDSYGLITHTRATINPGVDGTNR----IEST 413 QLTREVYTDPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSBIBFYTTRA 359 GADLANYYAQVYGVPYASFTL -- LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP 474 1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMAYKDYLRMSEGENPELFGNP DLIDOKITDSVRKTALAGLOGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDP VAXIPSFAISGOEVPLLSVYAQAANLHLILLENDASIFGAEWGFTPGEISTFYDRQVTRTA Gaps 42; Length 1157; Match 51.7%; Score 3126; DB 2; Length 11: Local Similarity 52.3%; Pred. No. 2.9e-197; Les 619; Conservative 195; Mismatches 327; Indels 120 121 180 181 241 301 Query Match 240 300 360 Matches ð å δ 윱 셤 윱 셤 8 & ò 8 Š δ 셤

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2: /cgn2_6/ptodata/1/pubpaa/PCT_PMW_PUB_pep:*
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Description	Sequence 1, Appli	4	4	Sequence 2, Appli	Sequence 2, Appli	2, 1	Sequence 72, Appl	28,	Sequence 6, Appli		Sequence 76, Appl	Sequence 7, Appli	Sequence 63, Appl	Sequence 23, Appl
SUMMARIES	US-10-089-678-1	US-10-414-637-4	US-10-606-320-4	US-10-032-717-2	US-10-414-637-2	US-10-606-320-2	US-10-099-285-72	US-10-428-961-28	US-10-614-524-6	US-10-099-285-74	US-10-099-285-76	US-09-988-462-7	US-10-428-961-63	US-09-826-660-23
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Score	6044	3263.5	3263.5	3246.5	3246.5	3246.5	3100.5	3100.5	2884.5	2825.5	2710	2519.5	2457	2454.5
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15 US-10-428-961-38 15 US-10-614-524-2 9 US-09-073-873-10 9 US-09-873-873-12 9 US-09-873-873-12	10 US-09-997-914-10 10 US-09-997-914-12 10 US-09-997-914-14 14 US-10-365-645-10 14 US-10-365-645-12	14 US-10-365-645-14 16 US-10-672-163-10 16 US-10-672-163-12 16 US-10-672-163-14 9 US-09-973-26 10 US-09-997-914-26	14 US-10-365-645-26 16 US-10-672-163-26 9 US-09-756-526A-2 14 US-10-345-020-2 14 US-10-342-821-2 9 US-09-977-914-28	14 US-10-365-645-28 16 US-10-672-163-28 19 US-9913-313-34 14 US-10-365-645-34 14 US-10-099-285-70 9 US-09-826-660-6 12 US-09-837-961-8
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ALIGNMENTS

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Sequence 1, Application US/10089678

Sequence 1, Application US/10089678

Publication No. US20030017967A1

GENERAL INFORMATION:
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GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NOKIOUS ORGANISM-CONTROLLING AGENT AND METHOD
FILE REPERENCE: Q68821

CURRENT APPLICATION NUMBER: US/10/089,678

CURRENT FILING DATE: 2002-05-02

PRIOR PEPLICATION NUMBER: PC1/JP01/06660

PRIOR FILING DATE: 2000-03

PRIOR FILING DATE: 2001-08-03

PRIOR FILING DATE: 2001-08-03

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PATENTIN Version 3.1

SEQ ID NOS: 3
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Best Local Similarity 100.0%; Pred. No. 0;
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US-10-032-717-4; Sequence 4, Application US/10032717

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                                                        APPLICANT: Nicholas B. Duck
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Peng
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Rain
APPLICANT: Theodore W. Rain
APPLICANT: Lynn B. Sims
TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO. 4.0
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Best Local Similarity 53.4%; Pred. No. 3e-258;
Matches 667; Conservative 178; Mismatches 284; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                TYPB: PRT ORGANISM: Bacillus thuringiensis
GENERAL INFORMATION:
                                              APPLICANT: Andre R. Abad APPLICANT: Nicholas B. Duck
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                              BTPIS-SSTVQTGIGIVGQVLGALGVPPAGQIASPYSPIVGQLWPSSTVSVWEMIMKQVR
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APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Xiang Feng
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Thom E. Sime
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/414, 637
CURRENT PILING DATE: 2003-04-16
PRIOR FILING DATE: 2001-10-23
PRIOR PLILING DATE: 2001-10-23
PRIOR PLILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
SOFTWARE: PASESEQ for Windows Version 4.0
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Best Local Similarity
Matches 667; Conserva
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                                            -----TLKYNPVSK 456
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                                                                                      ------RIPPE--NEPLSRGYSHRLSHITSYSPSKNASSPARYGNLPVPAWTHRS
                                                                                                             RINGENGWICSIGIEVAEGDVLFKDRSLRLISARRIDIETYPTYLYQQIDESLLKPYTRY
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Sequence 2, Application US/10032717
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Parm B. Simme
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 357194237005
FILE REFERENCE: 357194237005
CURRENT PILING DATE: 2001-10-23
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US-10-032-717-2
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Best Local Similarity 53.4%; Pred. No. 3e-258;
Matches 667; Conservative 178; Mismatches 284; Indels 119;
                                                                                                                                  1126 -----DQTSYITKTVEFTPSTEQVWIDMSETEGVFNIESVELVLEBE 1167
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Publication No. US20040091505A1
GERREAL INFORMATION:
APPLICANT: Ronald D. Flannagan
APPLICANT: Renal Herraman
APPLICANT: Refael Herraman
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Activity
TITLE OF INVENTION: Activity
TITLE OF INVENTION: Activity
FILE REPERENCE: 35718/263948
CURRENT FILING DATE: 2002-06-25
FRIOR APPLICATION NUMBER: 60/460,787
FRIOR APPLICATION NUMBER: 60/460,787
FRIOR APPLICATION NUMBER: 60/460,787
FRIOR FILING DATE: 2003-04-04
NUMBER: PABLES OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTI
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                         TETLIFNICDDDT-GVLSA--
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US-10-606-320-4
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ORGANISM:
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APPLICANT: Kiang Peng
APPLICANT: Knald D. Plannagan
APPLICANT: Tonald D. Plannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
TITLE OF INVENTION: Genes Encoding No. US20030177528Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
PRIOR PLLING DATE: 2003-04-16
PRIOR PLLING DATE: 2001-10-23
PRIOR PLLING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 48
SOFTMARE: PastSEQ for Windows Version 4.0
SSEQ ID NO 2
FENNING 2
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53.7%; Score 3246.5; DB 14; Length 1206;
Best Local Similarity 53.4%; Pred. No. 7.5e-257;
Matches 665; Conservative 172; Mismatches 290; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/10414637; Publication No. US20030177528A1; GENERAL INFORMATION: APPLICANT: Andre R. Abad
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PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1206
                                                                                                                                , ORCANISM: Bacillus thuringiensis US-10-032-717-2
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                                               S--ISSARYIRHWAGHQISYHRVSRGSNLQQMYGTNQNLASTSTFDFTNYDIXKTLSKDA 414
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Best Local Similarity 53.4%; Pred. No. 7.5e-257;
Matches 665; Conservative 172; Mismatches 290; Indels 119;
                                                            APPLICANT: Rafael Hermann
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James R. Presnail
APPLICANT: James F. H. Wong
APPLICANT: James F. H. Wong
APPLICANT: Genes Encoding Proteins With Pesticidal
ITILE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REPREMENT 35718/263948
CURRENT APPLICATION NUMBER: 60/31,786
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Bacillus thuringiensis
                                APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Plannagan
APPLICANT: Rafael Herrwann
APPLICANT: Theodore W. Kahn
US20040091505A1
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Best Local Similarity 52.0%; Pred. No. 6.9e-245;
Matches 615; Conservative. 196; Mismatches 330; Indels
                         PILLING DATE: «Unknown:
PILLING DATE: «Unknown:
PILLING DATE: «Unknown:
PILLING DATE: 1—UUL-1997
APPLICATION NUMBER: US 08/674,002
PILLING DATE: 1—UUL-1996
ATTORNEY/ABRATI INFORMATION:
NAME: SANGER: JS M. 39,355
REFERENCE/DOCKET NUMBER: NA-701C2
TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1156 anino acids
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; SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-099-285-72
                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                   APPLICATION NUMBER:
   PRIOR APPLICATION DATA
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| SEKAGKYRVRLRYATDADIVLHVNDA----QIQMPKTMNPGEDLTSKTFRVADALTTL 626
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                                                                                                                               KDALQTSVTDYQVNQAANLVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRI 749
                                                                                                                                                                                                                             NGENGNMSSDSHAPSFHIDTGEIDLNENTGIWVVPKIPTTNGYATLGNLELVEEGPLSGE 929
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                                                                             NGENGWIGSTGIEVARGDVILFKDRSIRITSAREIDTETYPTYLYQQIDESLIKPYTRYKI
                                                                                                                                               KGPIGSSQDLBIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALEN
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Publication No. US20030105319A1
GENERAL INFORMATION:
Micker, Carol
Micker, Carol
Marva, Kenneth E.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OP INVENTION:
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
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PAPLICATION NUMBER: US/10/099,285
PILING DATE: 15-Mar-2002
CLASSIFICATION: «UNKNOWN»
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
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                                                                                                                                                                                                                                                                        360 GLPLNNTBYLBYWVCHSIKYKNTNASSALBRNYGTITSNKIKY---YDLANKDIPQVRSL 416
                                                                                                                                                                                                                                                                                             360 -PPV-SSNPMDYWSGHILRRSYLNDSAVQEDSYGLITTTRATINPGVDGTNR----1EST 413
                                                                                                                                                                                                                                                                                                                                     GADLANYYAQVYGVPYASFTL -- LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP 474
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                                                                                                      LVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVAE
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                              DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLKNRNDTRARSVVVTQYIALBLDP
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Sequence 20, Application US/10428961

Publication No. US20030237111A1

GENERAL INPORMATION:
APPLICANT: Baum, James A.
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Amy J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
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APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
FULNE OF INVENTION: Polymuclectides, Compositions, and Methods of Use (Amended)
FILE RERERENCE: MCC0201-1

CURRENT APPLICATION NUMBER: US/10/428,961

FRIOR PILING DATE: 2000-09-13
FRIOR PILING DATE: 2000-09-13
FRIOR PILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.2
SEQ ID NO 28
SEQ ID NO 28
                                                                                                                                                                                                                                                                                             ARKRGASEKAYYAAKQAIDRLFADYQDQKLANGGVEMSDMLAAQNLVQSIPYVYNDALPEI 1005
                                                                                                                                                                                                                                                                                                                                                      PGMNYTSFTELTNRLOOAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVOOLSDTSVLVIP 1065
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 SST SSEYFIDELIFYNDAREAEBLEAAKKAVANLFTRTRDGLQVAVTDYQVDQAAN 698
                                                                                                         GDVLFKDRSLRLTSARBIDTBTYPTYLYQQIDESLLKPYTRYKLKGFIGSSQDLBIKLIR 825
                                                                                                                       HHYVHLVKNVPDNLVSDTYSDGSCSGINRCDEQHQVDWQLDAEHHPMDCCEAAQTHEFSS 874
                                                                                                                                                                                                                                  HIDTGRIDIMENTGINVVPKIPTTNGYATLGNLELVERGPLSGETLERAQQQEQQWQDKM 945
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                                                                                                                                                                                                                                                                                                               HRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMSSDSHAFSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1126 DQTSYITKTVEFTPSTEQVWIDMSRTEGVFNIBSVELVLEEB 1167
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595 LEVIISGIRIYSINVNKIMNKGDDLIFNIFDLATIGIAFIFSNYSDSLIVGADSFASGGE
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 1S/10/099,285
FILING DATE: 15-MAr-2002
CLASSIFICATION: <UNKNOWN>
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APPLICATION NUMBER: 09/002,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 74, Application US/10099285; Publication No. US/2003019319A1 GENERAL INFORMATION: APPLICANT: Schnepf, H. Ernest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wicker, Carol
Narva, Kenneth E.
Walz, Michelle
Stockhoff, Brian
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                 APPLICANT: Mathieu, Evaluation Applicant: Canada Applicant: Mathieu, Evaluation Applicant: Vanneste, Stijn
APPLICANT: Vanneste, Stijn
APPLICANT: Vanneste, Stijn
APPLICANT: Vanneste, Stijn
TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
FILE REFRENCE: NEWFISUS2
CURRENT PILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US/09/739,243
PRIOR APPLICATION NUMBER: 60/173387
PRIOR PILING DATE: 1999-12-18
PRIOR PILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 VAKIPSFAI----SGQEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTFGEISTFYDRQV
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Matches 578; Conservative 200; Mismatches 365; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.7%; Score 2884.5; DB 19
49.1%; Pred. No. 3.8e-227;
                                                                                                                             Sequence 6, Application US/10614524 Publication No. US20040016020A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                            APPLICANT: Arnaut, Greta
APPLICANT: Boets, Annemie
APPLICANT: Damme, Nicole
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952 SEKAYYAAKQAIDRLFADYQDQKINSGVEMSDMLAAQNIVQSIPYVYNDALPRIPGMNYT 1011
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                                                                                                                                                                                                                                                816
                                                                                                                                                                                                                                                                                        891
                                                                 BLYPNEKRMGWDAVKEAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVAEGDVLFKD 772
                                                                                                                                               RSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFIGSSQDLEIKLIRHRANQIV 832
                                                                                                                                                                                                                                                                                                             892 IDLNENTGIWVVPKIPTTNGYATLGNLELVEEGPLSGETLERAQQQEQQWQDXMARKRGA 951
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581 FFVTRGGTTINNFRFTRTMNRGQESRYBSYRTVBFTTPFNFTQSQDIIRTSIQGLSGNGE
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ADDRESSER: Saliwanchik, iloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
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PGMNYTSPTELTNRLOGAWNLYDLRNAIPNGDPRNGLSDWNATSDVNVQQLSDTSVLVIP 1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1005
                                                                                          HIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVEEGPLSGETLERAQQQEQQWQDKW 945
HHKVHLVKNVPDNLVSDTYSDGSCSGINRCERQHQVDVQLDABDHPKDCCBAAQTHBFSS
                                                                                                                                                                                                                                  869 YIHTGDIANASVDQGIWVVLQVRTTDGYATIGALIELVBVGPLSGBSLBRBQRDNAKWNBBV
                                                                       GDVLPKDRSLRLTSARRIDTBTY PTYLYQQIDBSLLKPYTRYKLKGFIGSSQDLBIKLIR
                                                                                                                                          HRANOIVKUVPDNILLPDVLPVNSCGGIDRCSBQQYVDANLALENNGENGNMSSDSHAPSP
                                                                                                                                                                                                                                                                                    946 ARKRGASEKAYYAAKQAIDRLFADYQDQKINSGVEMSDMLAAQNIVQSIPYVYNDALPBI
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Sequence 76, Application US/10099285

Publication No. US2003105319A1

GENERAL INCOMPATION:

APPLICANT: Schnepf, H. Ernest

Warva, Kenneth E.

Walz, Michelle

Stockhoff, Brian

Multer-Cohn, Judy

TITLE OF INVENTION: Toxins Active Against Pests

NUMBER OF SEGUENCES: 105

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainswille
STATE: Plorida
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APPLICATION NUMBER: US/10/099,285
FILING DATE: 15-Mar-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE: «Unkmown»
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REPERENCE/DOCKET NUMBER: MA-701C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/002, 285
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MEDIUM TYPE: Floppy disk
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ZIP: 32606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POVRSLGADLANYYAQVYGVPYASPTLLDKNYGSGSVGGPTYSKPHTTMQVCTQNYNTID 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTN--LRLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGAD 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 BLFGNPETFISSSTVQTGIGIVGQVLGALGVPPAGQIASFYSFIVGQLWPSSTVSVWEMI 114
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                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                          DB 14; Length 1150;
                                                                                                                                                                                                                                                                                                                                                                                                           47;
                                                                                                                                                                                                                                                                                                                                                                        Query Match
46.7%; Score 2825.5; DB 14; Lengtl
Best Local Similarity 48.6%; Pred. No. 2.6e-222;
Matches 574; Conservative 197; Mismatches 364; Indels
                                                                                  NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REGISTRATION NUMBER: 39,355
TELECOMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEPAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-UTL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-UTL-1996
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
                                                                                                                                                                                                                                    LENGTH: 1150 amino acids
                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                         US-10-099-285-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355
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PADYQDQKLINSGVEMSDMLAAQNLVQSIPYVYNDALPEIPGMNYTSFTELTNRLQQAWNL 1026
                                                                                                                                                                                                    VTARKEGVGDGYVIIRDGANQTETLIFNICDDDTGVLSADQTSYITKTVBFTPSTEQVWI 1146
                                                                                                                                                                                                                                                                   1054 VTAEKVGGGGGGYVTIRDGAHHTETLTFNACDYDINGTYVTDNTYLTKEVIFYSHTEHMWV 1113
                                                                             PTTNGYATLÆNLELVEEGPLSGETLERAQQQEQQWQDKMARKRGASEKAYYAAKQAIDRL
SCGGIDRCSEQQYVDANLALENNGE-NGNMSSDSHAPSFHIDTGEIDLNENTGIWVVFKI
                YDLRNAI PNGDFRNGLSDWNATSDVNVQQLSDTSVLVI PNWNSQVSQQFTVQPNYRYVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-00. US20030046726A1-2001
CLASSIFICATION: «Unchown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/971,027
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology,
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                 1114 EVNETEGAPHIDSIEPVETEK 1134
                                                                                                                                                                                                                                                                                                                  DMSETEGVFNIESVELVLEER 1167
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Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Bllis J.
Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YHQPRREMTLLVLDLVALPPNYDTRTYPIBTTAQLTREVYTDPIVFNRBTSGGF----CR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RWSLNSDISPSEVESAVIRSPHLPDILSEIBPYTTRAGLPLNNTRYLEYWGHSI--KYK 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WINASSALERNYGTITSNKIKYYDLANKDIPQVRS---LGADLANYYAQVYGVPYASFTL 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDRIP--PENEPLSRGYSHRLSHITSYSF 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RABEDLDVAKKAVNGLFTSKKODALQTSVTDYQVNQAANLVECLSDBLYPNEKRMLMDAVK 729
                                                                                                                                                                                                                                                                                                                                 93 SFYSFIVGQLWPSSTVSVWEMIMKQVEDLIDQKITDSVRKTALAGLQGLGDGLDVYQKSL 152
                                                                                                                                                                                                                                                                                                                                                                                            KNWLENRNDTRARSVVVTQYIALELDPVAKIPSPAISGQ-----EVPLLSVYAQAANLHL 207
                                                                                                                                                                                                                                                                                                4 NPNINECIPYNCLSNPEVEVLGGERGNVRT-----GLOTGIDIVAVVGALGGPVGGILT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NWNYKDYLRMSEGENPEL-----PGNPETPISSSTVQTGIGIVGQVLGALGVPPAGQIA
                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                    Length 1134;
                                                                                                                                                                                                    Query Match
44.8%; Score 2710; DB 14; Length Best Local Similarity 48.1%; Pred. No. 7.9e-213;
Matches 559; Conservative 195; Mismatches 345; Indels
                                                                             TYPE: amino acide

STRANDEDNESS: sincle

TYPOLGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 76:

US-10-099-285-76
                TELEPHONE: (352) 375-8100
TELEPAX: (352) 372-5800
FELECOMMUNICATION INFORMATION
                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1134 amino acide
                                            INFORMATION FOR SEQ ID NO: 76:
                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237
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APPLICANT: Baum, James A.
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih. Rei
APPLICANT: Chu, Chih. Rei
APPLICANT: Chu, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Amy J.
APPLICANT: Rupar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: NUMBER: US/10/428,961
CURRENT APPLICATION NUMBER: 09/661,322
PRIOR PILING DATE: 2000-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
                                                                                                                                                                 1051 CGYILRVTAYKEGYGEGCVTIHEIENNTDELKPKNREBEEVYPTDTGTCNDYTAHQGTAG 1110
                                                                                                                                                                                                                                                                                   | |: | | :: | | 111 CADACHSRNAGYEDAYEVDTTASVNYKPTYBEBTYTDVRRDNHCEYDRGYVNYPPVPAGY 1170
                                                                                       QAIDRLFADYQDQXLMSGVEMSDMLAAQMLVQSIPYVYNDALPRIPGMNYTSFTELTNRL 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1021 QQANNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIPNWNSQVSQQFTVQPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         913 VESPIGRCGEPNRCA--PHFEWNPDLDCSCRDGERCAHHSHHFSLDIDVGCTDLHENLGV
                                                                                                        1114 -----NICDDDTGVLSAD--QTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIDOKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALBLDFV
                               WVVPKI PTTNGYATLGNLBLVEBGPLSGETLERAQQQEQQWQDKMARKRGASEKAYYAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSPNNQNEYRILDASSSTSVSDNSVRYPLANDQTTTTLQNMNYKDYLRMSEGENPELPGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.7%; Score 2457; DB 15; Length 1227; 42.8%; Pred. No. 5.4e-192;
                                                                                                                                                                                                           1081 YRYVLRVTARKEGVGDGYVIIRDGANQTETLTP-------
                                                                                                                                                                                                                                                                                                                                               Query Match 40.7%; Score 2457; DB 15; Best Local Similarity 42.8%; Pred. No. 5.4e-192; Matches 541; Conservative 197; Mismatches 392;
                                                                                                                                                                                                                                                                                                                                ITKTVEPTPSTEQVWIDMSETEGVPNIESVELVLEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 63, Application US/10428961; Publication No. US20030237111A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.2
SEQ ID NO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1227
                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-428-961-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAVIRSPHLFDILSBIEFYTTRAGLPLNNTEYLEYWVCHSIKYK-----NTNASSALER 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SINPVILE-----PASEDVYRTESYAGVLLWGIYLEPIHGVPTVRFNFTNPQNISDR-G 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFTYSKPHTTMQVCTQNYNTIDBIPPB--NBPLSRGYSHRLSHITSYSFSKNASSPARYG 506
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41.7%; Score 2519.5; DB 10; Length 1207;
Best Local Similarity 44.3%; Pred. No. 3.9e-197;
Matches 548; Conservative 178; Mismatches 372; Indels 139; Gaps
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SEQUENCE DESCRIPTION: SEQ ID NO:
TELEPHONE: (919)541-8587
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
                                                                          TYPE: amino acid
TOPOLOGY: linear
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LTREVYTDPIVFNRETSGGPCRRWSLNSDISPSEVESAVIRSPHLFDILSEIEFYTTRAG 360
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                                                                    361 LPLANTEYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKYYDLANKDIPQVRSLGADL
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                                                                                                                                         179 LSRGYSHRLSHITSYSFSKNASSPARYGN---LPVFAWTHRSADVTNTVYSDKITQIPVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 40.6%; Score 2454.5; DB 9; Length 1186; Best Local Similarity 43.1%; Pred. No. 8.3e-192; Matches 536; Conservative 191; Mismatches 382; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-23
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596 FVTISGTRIYSINVNKTMAKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGEV 655 	656 YVDKFELIPVNATFRAREDLDVAKKAVNGLFTSKKD-ALQTSYTDYQVNQAANLVECLSD 714 	715 ELYPNEKRMLWDAVKEAKRLVQARNILLQDTGFNRINGENGWTGSTGIEVAEGDVLFKD 772 689 EPCLDEKKELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGGDDVFKE 748	773 RSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFIGSSQDLEIKLIEHRANQIV 832 	833 KNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMSSDSHARSFHIDTGEI 892 	893 DIAMENTGIWVVFKI PTINGYATLGANLELVEBGPLSGETLERAQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ	953 EKAYYAAKQAIDRLFADYQDQKLANSGVEMSDMLAAQXLVQSIPYVYNDALPEIPGANYTS 1012 	013 FTELTNRLQQAMNLYDLRNAIPNGDFRNGLSDMNATSDVNV-QQLSDTSVLVIPNMNSQV 1071 	72 SQOFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDD 1118 :	19 DTGV	1130YITKTVBFTPSTEQVMIDMSETEGVFNIBSVELVLABB 1167 - - - - - - - - - - -	
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-07-811-180A-2

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US-08-15-203-2

US-08-272-887-2

US-08-272-887-2

US-08-379-656B-5

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US-08-379-656B-5

US-08-471-177-5

US-09-471-177-5

US-09-661-322A-28

US-09-661-322A-28

US-09-661-322A-28

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US-09-661-322A-28

US-09-68-477-74

US-08-880-685-2

US-09-002-285-76

US-08-880-685-2

US-09-002-685-7
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                                                                                                                                                                                                                                                                                                                                                                         389414 segs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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APPLICANT: Payley, Jewel M.
APPLICANT: Bagley, Angela L.
TITLE OF INVENTION: Controlling Acarides
TITLE OF INVENTION: Controlling Acarides
CORRESPONDENCE ADDRESS:
ADDRESSER: David R. Saliwanchik
Sequence 4, A Sequence 2, A Sequence 7, A Sequence 7, A Sequence 7, A Sequence 8, A Sequence 8, A Sequence 23, Sequence 23, Sequence 23, Sequence 23, Sequence 23, Sequence 24, A Sequence 24, A Sequence 14, A Sequence 14, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/876,280
FILING DATE: 19920430
CLASSIFICATION: 514
ATTOMENY/AGENT INPORMATION:
NAME: SAliwanchik, David R.
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REJECOMMUNICATION NUMBER: M/S 104
TELECOMMUNICATION NUMBER: M/S 104
TELERPAX: 904-372-5800
TELERPAX: 904-372-5800
SEQUENCE CHARACTERISTICS:
TENEVALLE CHARACTERISTICS:
TENEVALLE CHARACTERISTICS:
                          US-07-951-715A-7
US-08-459-448A-7
US-08-459-595A-7
US-08-459-544-7
US-08-459-444-7
US-09-547-422-7
US-09-547-422-7
US-09-561-803-9
US-09-661-322A-63
US-09-661-322A-63
US-09-826-660-23
US-09-826-660-23
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STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: PSSOC
; IMMEDIATE SOURCE:
; CLONE: B. coli NM522(pMYC2320) NRRL B-18769
US-07-876-280-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2421 N.W. 418t Street, Suite A-1 CITY: Gainesville STATE: FL
                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                            US-07-876-280-30
; Sequence 30, Application US/07876280
; Patent No. 5262158
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1157 amino acida
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
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HYPOTHETICAL: YES
  HYPOTHETICAL: )
ANTI-SENSE: NO
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2441.5
2237.5
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GENERAL INFORMATION:
APPLICANT: Poncerrada, Luis R
APPLICANT: Payne, Jewel M
APPLICANT: Payne, Jewel M
APPLICANT: Sick, August J
TITLE OF INVENTION: No. 5366892el Coleopteran-Active Bacillus
TITLE OF INVENTION: Coleopteran-Active and a No. 5366892el Gene Encoding
TITLE OF INVENTION: Coleopteran-Active Toxin
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
1019 RLQQAMNLYDLRNAIPNGDFRNGLSDWATSDVNVQQLSDTSVLVIPNWNSQVSQQFTVQ 1078
1009 RLQQAMNLYDQRNAIPNGDFRNGLSNWNATPGVEVQQINHTSVLVIPNWDEQVSQQFTVQ 1068
                                                                                1069 PNORYVLRVTARKEGVGNGYVSIRDGGNQSETLIFFSASDYDTNGVYNDOTGYTKTVIFI 1128
                                                               PNYRYVLRVTARKEGVGDGYVI IRDGANQTETLIFNI CDDDTGVLSADQTSY ITKTVRFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRIES READABLE FORM:

MEDIUM TYER: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Batenflin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,180A
FILING DATE: 19920102
CLASSIFICATION: 435
ATTORNEY/AGRAT INPORMATION:
NAME: SAIWANGHIK, Roman
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEBROAK: 904-372-5800
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Best Local Similarity 66.1%; Pred. No. 2.3e-285;
Matches 773; Conservative 144; Mismatches 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TM) - 11 LIBRARY OF LUIS
                                                                                                                                                 | |:|:||:|||| | |||||| | PYTDQMMIEISETEGTFYIESVELIVDVE 1157
                                                                                                                                PSTEQUWIDMSETEGUFNIESVELVLERE 1167
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                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSER: Roman Saliwanchik
STREET: 2421 N.W. 41st Street, Ste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
                                                                                                                                                                                                                  RESULT 2
US-07-1212-180A-2
; Sequence 2, Application US/07812180A
; Patent No. 5366892...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: AMINO ACID
STRANDEDWESS: single
TOPOLOGY: linear
MOLEGULE TYPE: protein
HYPOTHETICAL: YES
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LIBRARY: FONCERRADA
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US-07-812-180A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                     SIPSFAVSGHEVLLLAVYAQAVNLHILLLRDASIFGEEWGFTPGEISRFYNRQVQLTAE
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                                                     Gaps
                                                 14;
                      Length 1157;
                  Query Match 66.3%; Score 4007; DB 1; Length 1 Best Local Similarity 66.1%; Pred. No. 2.3e-285; Matches 773; Conservative 144; Mismatches 238; Indels
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Gaps

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61 ETFISSSTVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVED 120
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                                                                                                                                                  APPLICANT: Michaels, Tracy Ellis
APPLICANT: Poncerrada, Luis
APPLICANT: Poncerrada, Luis
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Process for Controlling Scarab Pests
TITLE OF INVENTION: with Bacillus thuringiensis Isolates
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,468
| |:|:||:|||| | |||||||:::|
PYIDQMWIBISBIBGTPYIBSVBLIVDVB 1157
                                                                                                                                                                                                                                                                   ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REJECRATION NUMBER: 31,794
REJECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
INBORDANCE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/014,941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/014,941
PILLING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
PILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/808,316
PILING DATE: 16-DEC-1991
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
                                                                                                   Sequence 2, Application US/08315468
Patent No. 5554534
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: PSSOC
IMMEDIATE SOURCE:
LIBRARY: Lambdagem (TM) - 11
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 773; Conservat
                                                                                                                                                                                                                                                                                      STREET: 2421 N.W. CITY: Gainesville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                    32606
                                                                    RESULT 3
US-08-315-468-2
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                                                                    LIDOKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALRLDFV
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                                                                                                      GENERAL INFORMATION:
APPLICANT: Uyeda, Kendrick A.
APPLICANT: Bradfisch, Gregory A.
TITLE OF INVENTION: Process for Controlling Lepidopteran Pests
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1157;
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66.3%; Score 4007; DB 3; Length 1

Best Local Similarity 66.1%; Pred. No. 2.3e-285;

Matches 773; Conservative 144; Mismatches 238; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; INMEDIATE SOURCE:
; CLONE: E. coli NM522 (pMYC1638), NRRL B-18751
US-07-941-650A-2
1129 PYTDQMWIBISETEGTFYIBSVELIVDVE 1157
                                                                                                                                                                                                   ADDRESSER: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite
CITY: Galnesville
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,650A
FILING DATE: 19920908
CLASSIFICATION: 435
CLASSIFICATION WASTE: US 07/758,020
APPLICATION NUMBER: US 07/758,020
FILING DATE: 12-EBP-1991
PRIOR APPLICATION NUMBER: US 07/658,935
FILING DATE: 21-EBP-1991
PRIOR APPLICATION NUMBER: US 07/658,935
FILING DATE: 16-ABP-1991
ATTORNEY/AGENT INFORMATION:
NUMBE: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
FRIEGCYMUNICATION NUMBER: 31,794
FRIEGCYMUNICATION NUMBER: 31,794
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STRAIN: kumamotoensis
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                           Sequence 2, Application US/07941650A Patent No. 6294184
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TOPOLOGY: linear
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MEDIUM TYPE: Floppy
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Best Local Similarity
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181 SSIPSPAVSGHEVLLLAVYAQAVNIHLLLLENDASIPGEEWGFTPGEISRFYNRQVQLTAE 240
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                                               LIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFV 180
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SIPSFAVSGHEVILLAVYAQAVNIHILLILRDASIFGEEWGFTFGEISRFYNRQVQLTAE
                                                                                                              YSDYCVKWYKIGLDKIKGTTSKSWI.NYHQPRREMTLIVLDLVALPPNYDTHMYPIETTAQ
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BLTREIPTDFV-----GSYVTGQSSTLISWYDMIPAALPSFSTLEN-LLRKPDFPTLL 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER REALISE FORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PRE-BASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/915,203
FILING DATE: 1992073
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/K 301
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUIRICE CHARACTERISTICS:
                                                               APPLICANT: Obba, Michio
APPLICANT: Iwahana, Hidenori
APPLICANT: Iwahana, Hidenori
APPLICANT: Suzuki, No. 5359048ukazu
APPLICANT: Suzuki, No. 5359048ukazu
APPLICANT: Sakanaka, Kazunobu
APPLICANT: Asanaka, Kazunobu
APPLICANT: Asano, Shouji
APPLICANT: Kawasugi, Tadaaki
TITLE OP INVENTION: No. 5359048el Microorganism and
NUMBER OP ESQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                              ADDRESSER: David R. Saliwanchik
STREF: 2421 N.W. 41st Street, Suite
CITY: Gainesville
STATE: FL
2, Application US/07915203
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AMINO ACID
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/272,887
FILING DATE: 08-UUL-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/915,203
FILING DATE: 23-ULL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
                                  ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CTTY: Gainesville
STATE: FL
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/K 301
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                   ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 1149 amino acids
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
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                      SEI BFYTTRAGLPLNNT-EYLEYWVGHSI KYKNTNASSALBRNYGTI TSNKI KYYDLANK
                                                                                                DI POVRSLGADLANYYAQVYGVPYASFITLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNT
                                                                                                                                   DIYRV--VWTYIGRYTNSLLGVNPVTF-YPSNNTQK-----TYSKP----KQFAGGIKT
                                                                                                                                                                              469 ID---EIPPENBPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVPAWTHRSADVTNTVY
                                                                                                                                                                                                526 SDKJTQIPVVKAHTLVSGTTVIKGPG-PTGGNILKRTSSGPLAY---TSVSVKSPLSQRY
                                                                                                                                                                                                                                                                                634 TPSNYSDSLTVGADSPASGGEVYVDKPELIPVNATFRAEEDLDVAKKAVNGLFTSKKDAL
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                                                                                                                                                                                               408 DIYRV----KQFAGGIKT
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                                                                                                                                1 MSPNWQNBYBIIDALSPISVSDNSIRYPLANDQTNTLQNMNYKDYLKMTBSTNABLSRNP
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                                                                                Gaps
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                                                 Length 1149;
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                                               60.6%; Score 362.5; DB 1;
ilarity 63.8%; Pred. No. 4.6e-260;
Conservative 109; Mismatches 257;
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                                                                 Similarity
                                                 Query Match
Best Local Simil
Matches 752; (
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Kawasugi, Tadaaki ENTION: No. 5747450el Microorganism and Insecticide

Hori, Hidetaki Asano, Shouji

APPLICANT:
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APPLICANT:

INVENTION:

Obba, Michio Iwahana, Hidenori Sato, Relichi Suzuki, No. 5747450ukazu Ogiwara, Katsutoshi Sakanaka, Kazunobu

Sequence 2, Application US/08272887 Patent No. 5747450 GENERAL INFORMATION:

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180 VAKIPSFALSGQEVPLLSYXAQAANIHLLILADASIFGAEMGFTPGEISTFYDRQVTRTA 239
181 RINMGSFSQTNYETPLLPTYAQAASLHLLVMRDVQIYGKEMGYPQNDIDLFYKEQVSYTA 240
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                PatentIn Release #1.0, Version #1.25
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60.6%; Score 3662.5; DB 2
Best Local Similarity 63.8%; Pred. No. 4.6e-260;
Matches 752; Conservative 109; Mismatches 257;
                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,887
PILING DATE: 08-UUL-1994
APPLICATION NUMBER: US 07/915,203
PILING DATE: 23-UUL-1992
ATTORNEY/AGENT INFORMATION:
                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,44*
FILING DATE:
                                                                                                                                                                                     NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/K 301
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                              1149 amino acids
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                                                                                                                                                                                                                                                                                                                              amino acid
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US-08-789-449-2
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                                                                                            RARIRYASTINLRLFVTIS-----GTRIYSINVNKIMNKGDDLTFNTFDLATIGTA-F 633
 IDSGRELTYEN---YQSYSHRVSYITSFEIKSTGGTV--LGVVPIFGWTHSSASRNNFIY 509
                                                                                                                                                                                                                  QTSVTDYQVNQAANLVBCLSDELYPNEKRALMDAVKBAKRLVQARNLLQDTGFNRINGEN
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                                                                                                                                                                           GSSQDLEIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALENNGEN
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                                 SDKITQIPVVKAHTLVSGTTVIKGPG-FTGGNILKRTSSGPLAY---TSVSVKSPLSQRY
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TITLE OF INVENTION: No. 5824878el Microorganism and Insecticide
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NICDDDTGVLSTDQTSYITKTVBFTPSTEQVWIDMSETE 1145
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohba, Michio
Iwahana, Hidenori
Sato, Relichi
Suzuki, No. 5824878ukazu
Ogiwara, Kateutoshi
Sakanaka, Kazunobu
Hori, Hidetaki
Asano, Shouji
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.2%; Score 3152; DB 1; Length 1. Best Local Similarity 54.0%; Pred. No. 1.4e-222; Matches 653; Conservative 179; Mismatches 294; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Poncerrada
                                                                                                                                                                                                                                                                                                                                                                                             ä
             NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERNICE/OCKET NUMBER: MA73.C2
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 amino acids
                                                                                                                                                                                                                                                                                                                                                                                           LambdaGEM-11 library of
                                                                                                                                                                                                                                                                                                                   ORGANISM: Bacillus thuringiensis STRAIN: kumamotoensis
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David
                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE: 50C
                                                                                                                                                                                                STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                      amino acid
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CLONE: 50C(b)
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ANTI-SENSE: NO
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US-08-315-468-4
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                 867 GNMSSDSHAFSFHIDTGEIDLMENTGIWIVPKIPTINGNATLGNLEFVEBGPLSGETLEW
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                                                                                           QTSVTDYQVNQAANLVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNR INGEN
                                                                                                              QTSVTDYQVNQAANLIECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRINGEN
                                                                                                                                                                 GWTGSTGIEVAEGDVLPKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFI
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APPLICANT: Michaels, Tracy Ellis
APPLICANT: Michaels, Tracy Ellis
APPLICANT: Poncertada, Luis
APPLICANT: Nava, Kenneth B.
TITLE OF INVENTION: With Bacillus thuringiensis Isolates
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEB: David R. Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1114 NICDDDTGVLSADQTSYITKTVRFTPSTEQVWIDMSETE 1152
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,468
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/014,941
FILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 07/808,316
FILING DATE: 16-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Gainesville STATE: PLANCE SUIMANCHIK STREET: 2421 N.W. 41st Street, Suimarchite STATE: PL COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08315468 Patent No. 5554534
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PRIOR APPLICATION DATA:
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           SVNASSNIQRLSIGIQTNTNLFILDRIEFIPVDETYBAETDLEAAKKAVNALPTNTKDGL
                                                                                                 ---PASGGEVYV-DKFELIPVNATFEABEDLDVAKKAVNGLFTSKKDAL
                                                                                       GWTGSTGIEVAEGDVLPKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGPI
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APPLICANT: VAN AUDENHOVE, KATRIEN
APPLICANT: VAN RIE, JEROGEN
APPLICANT: VAN ARSENGEN
APPLICANT: VAN ARSESEN, ROGE
TITLE OF INVENTION: INSECTICIDAL PROTEINS.
TITLE OF INVENTION: INSECTICIDAL PROTEINS.
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NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/532,547
FILING DATE: 06-DEC-1996
CICASSIFICATION: 0800
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08532547
Patent No. 5861543
GENERAL INFORMATION:
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ESVELIVDVE 1169
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                                                                                                                                                                                                                                               Length 1157;
                                                                                                                                                                                                                                               Query Match 51.7%; Score 3123; DB 2; Length 11 Best Local Similarity 52.3%; Pred. No. 1.9e-220; Matches 619; Conservative 195; Mismatches 327; Indels
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKST NUMBER: 21
FELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEPAX: (703) 205-8050
                                                                                    TELEX: 248345
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
TYPE: amino acid
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HOLECULE TYPE: protein
US-08-532-547-5
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                                                                                                            42;
                                                                           Length 1157;
                                                                                                            Indele
                                                                         3; DB 2;
1.9e-220;
                                                                                                            Matches 619; Conservative 195; Mismatches 327;
                                                                           Score 3123;
Pred. No. 1.9
                                                                           51.78;
          TOPOLOGY: linear
MOLECULE TYPE: protein
amino acid
                                                                                           Similarity
; TYPE: amin
; TOPOLOGY:
; MOLECULE TYPE
US-08-379-6568-5
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                                                                                                                                            MARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPE 1004
                                                                                                                                                             PHIDTGEIDLNENTGIWVVPKIPTTNGYATLGNIELVERGPLSGETLERAQQQEQQWQDK 944
                                                                                                          875 SYINTGDINASVDQGIWVVLKVRTTDGYATLGNLELVEVGPLSGESLEREQRDNAKWNAE 934
                           RHRANQI VKNVPDNILI PDVLPVNSCGCI DRCSEQQYVDANI.ALENNGENGNMSSDSHAFS
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APPLICANT: Jansens, Stefan
APPLICANT: Jansens, Stefan
APPLICANT: Van Audenhove, Katrien
APPLICANT: Peferoen, Marnix
TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STR
TITLE OF INVENTION: THEIR INSECTICIDAL PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22042
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,656B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFLICATION WOMEN: US/US/3/3/00020 AFLICATION WOREN: 23-WAR-1995
PRIOR APPLICATION WATA: APPLICATION WOBER: PCT/EP93/01820 FILING DATE: 12-JULY-1993
PRIOR APPLICATION DATA: EP 93400949.9 PRIOR APPLICATION WOMER: EP 93400949.9 PRIOR APPLICATION WOMER: EP 92402358.8 PRILNG PATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REPRENECA FOCKET UNMBER: 2121-104P
TELECOMUNICATION: (703) 205-8000
TELEFAX: (703) 205-8050
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08379656B Patent No. 5885571
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
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STATE: Virginia
COUNTRY: U.S.A.
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MSPNNQNEYE I LDASSSTSVSDNSVRYPLANDQTTTTLQNMNYKDYLRMSEGENPELPGNP
                                                   61 RTPISS-STVQTGIGIVGQVLGALGVPRAGQIASFYSPIVGQLWPSSTVSVWEMIMKQVB
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                                                      1005 IPGMYTSFIELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI
                                                                                                       PNWNSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVI IRDGANQTETLTFNI CDDDTGVLS
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APPLICANT: Lambert Stefan
APPLICANT: Jansens, Stefan
APPLICANT: Van Audenhove, Katrien
APPLICANT: Pefercen, Marmix
TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND
TITLE OF INVENTION: THEIR INSECTICIDAL PROTEINS
                                                                                                                                                           1125 ADQTSYITKTVEPTPSTBQVWIDMSETEGVFNIESVELVLEER 1167
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Best Local Similarity 52.3%; Pred. No. 1.9e-220;
Matches 619; Conservative 195; Mismatches 327;
                                                                                                                                                                                                                                                                                                                                                                              STREET: BIRCH, STEWART, KOLASCH & BIRCH STREET: 8110 Gatehouse Road, Suite 500 Bast CITY: Palls Church STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/01820
FILING DATE: 12-JULY-1993
FILING DATE: 12-JULY-1993
FILING DATE: 09-APR-1993
FILING DATE: 09-APR-1993
FILING DATE: 109-APR-1993
FILING DATE: 27-AUG-1992
ATTORNEY AGENT INFORMATION:
NAME: SVENBSON, LEGNAR'R.
NAME: SVENBSON, LEGNAR'R.
REGISTRATION NUMBER: 30,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 2121-106P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                     Sequence 5, Application US/08455838
Patent No. 6028246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (703) 205-8000
(703) 205-8050
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INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
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995 IPGINYBIYTELSDRLQQASYLYTSRNAVQNGDFNSGLDSWNTTMDASVQQDGNMFFVVL 1054
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                                                                                                                                                         360 GLPLANTEYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKY---YDLANKDIPQVRSL 416
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                                                                                                       QLTREVYTDPIVENPPANVGLCRRWGTNPYNTFSELENAPIRPPHLPDRLASLTISSNR-
                                                                                                                                                                           - PPV-SSNFMDYWSGHTLRRSYLNDSAVQEDSYGLITTTRATINFGVDGTWR---IRST
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                    OYSDYCVKWYNTGLDKLKGTNAASWLKYHOPRREWTLLVLDLVALPPNYDTRTYPIETTA
                                                                                     OLTREVYTDPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSBIEFYTTRA
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; Sequence 5, Application US/09471177
; Patent No. 6448226
; GENERAL INFORMATION:
APPLICANT: LAMBERT, BART
; APPLICANT: JANSENS, STEFAN
                  240
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SHWDAQVSQQLRVMPNCKYVLRVTRKVGGGDGYVTIRDGAHHQETLTFNACDYDVNGTY 1114
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PEPLICANT: JANSENS, STEPAN
APPLICANT: WA AUDENDOVE, KATRIEN
APPLICANT: VAN ALDENOVE, KATRIEN
APPLICANT: VAN RIE, JEROEN, MARNIX
APPLICANT: VAN ARSSEN, ROEL
TITLE OF INVENTION: INSETICIDAL PROTEINS.
TITLE OF INVENTION: INSETICIDAL PROTEINS.
TITLE OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: Palls Church
STATE: Virginia
COUNTRY: USA
ZIP: 220.
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                                                    1125 ADQTSYITKTVEFTPSTEQVWIDMSETEGVFNIRSVELVLERE 1167
                                                                        ZIF: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IR PC computable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (RPO)
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APPLICATION NUMBER: US/09/019,809
FILING DATE: 02-FEB-1998
CLASSIFICATION: 435
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NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8060
TELEPAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 248345
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
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1005 IPGMNYTSFTELTNRLQQAMNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI 1064
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                                                                                     533 PVVKAHTLVSGTTVIKGPGFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTN
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                                                                  GADLANYYAQVYGVPYASPTL - - LDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTIDBIPP
                                                                                                                                       475 ENEPLSRGYS-HRLSHITSYSFSKN-ASSPARYGNLPVFAWTHRSADVTNTVYSDKITQI
                                                                                                                                                            593 LRLFVTISGTRIYSINVNKTMNKGDDLTFNTP---DLATIG---TAPTFSNYSDSLTVGA
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; Sequence 72, Application US/09002285
; Patent No. 6369213
; Fatent No. 6369213
; GERRAL INFORMATION:
APPLICANT: Wicker, Carol
APPLICANT: Waler, Carol
APPLICANT: Waler, Machelle
APPLICANT: Wale, Michelle
APPLICANT: Wale, Michelle
APPLICANT: Wale, Michelle
APPLICANT: Wale, Michelle
APPLICANT: Wale, Dockhoff, Brian
APPLICANT: Waler-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N W 41st Street, Suite A-1
CITY: Gainesville
STREET: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                     707
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                                                                                                                           THURINGIENSIS STRAINS AND THEIR
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                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/471,177
APPLICANT: VAN AUDENHOVE, KATRIEN
APPLICANT: PERENGEN, MARNIX
APPLICANT: VAN ALSSEN, ROBL
TITLE OF INVENTION: INSECTICIDAL PROTEINS:
TITLE OF INVENTION: INSECTICIDAL PROTEINS:
TITLE OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNBER: US/09/019,809
FILLING DATE: 02-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: STENSON, LEGONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 31,330
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                  ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB PR Compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
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TELEPAX: (703) 205-8050
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PILING DATE
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-589-477-72
; Sequence 72, Application US/09589477
; Patent No. 6570005
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanch
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STATE: Florida
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CLASSIFICATION:
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                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,285
                                                                                                                                                                                                                                         NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REGISTRATION NUMBER: 39,355
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                                                                   TELEPHONE: (352) 375-8100
TELEFAX: (352) 375-5800
INFORMATION FOR SEQ ID NO: 72:
SEQUIBORE CHARACTERISTICS:
LENGTH: 1156 amino acids
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-002-285-72
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1006 PERNYTSFIELTNRIQOAWNLYDLRNAIPNGDFRNGLSDWNAISDVNVQQLSDISVLVIP 1065
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LVECLSDELYPNEKRMEMDAVKEAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVAE
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APPLICANT: Wicker, Carol
APPLICANT: Narva, Remeth B.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
TITLE OF INVENTION: Toxins Active Against Pests
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STREET: 2421 N.W. 418t Street, Suite A-1
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301 QLTREVYIDPIVFNPPANVGLCRRWGTNPYNTPSBLENAPIRPPHLFDRLANSLIISSNR- 359
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PELICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
CLASSIFICATION: 1-JUL-1997
CLASSIFICATION: NUMBER: US 08/674,002
APPLICATION UNMBER: US 08/674,002
FILING DATE: 1-JUL-1996
CLASSIFICATION: 1-JUL-1996
CLASSIFICATION: 39,355
REGISTRATION NUMBER: 39,355
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C1C1
TELECOMMUNICATION: TELEPHONE: (352) 375-8100
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 amino acids
                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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1066 NWNSQVSQQPTVQPNYRYVIRVTARKEGVGDGYVIIRDGANQTETLTPNICDDDTGVLSA 1125 PGMNYTSPTELTNRLQQAMNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIP 1065 946 ARKRGASEKAYYAAKQAIDRLPADYQDQKINSGVEMSDMLAAQNIVQSIPYVYNDALPEI 1005 825 882 874 814 GDVLFKDRSLRLTSAREIDTBTYPTYLYQQIDESLLKPYTRYKLKGFIGSSQDLEIKLIR 826 HRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQOYVDANLALENNGENGNMSSDSHAFSF 639 GVSTGSEYFIDRIBIIPVNPARRABEDLEAAKKAVANLFTRTRDGLQVNVTDYQVDQAAN 708 LVECLSDELYPNEKRMENDAVKRAKRLVQARNILLQDTGFNRING - - ENGWTGSTGIEVAE 1126 DQTSYITKTVEPTPSTEQVWIDMSETEGVPNIESVELVLEEE 1167 994 1006 ठे 셤 ò 셤 ò 셤 Š 셤 ð 윱 ठ 셤 ò è

Search completed: June 21, 2004, 13:40:18 Job time : 27 secs

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241 RYSDHCVQWINAGLNKIRGTGAKQWVDYNRFRREMYWVLDLVALFPNYDARIYPLETNA 300
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301 ELTREIFTDPV-----GSYVTGQSSTLISWYDMIPAALPSFSTLEN-LLRKPDFFTLL 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIPISS-STVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLWPSSTVSVWRMIMKQVE
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                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                              257;
                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 63.8%; Pred. No. 4.6e-260;
Conservative 109; Mismatches 257;
                                                                                                                                                                                                                                                                                                                                                                                                             60.6%; Score 3662.5; 63.8%; Pred. No. 4.6e
                                                                                                            US 08/272,887
                                                                                                                                           US 07/915,203
                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,444
                                                                                                                                                                                       NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/K 301
TELECOMMUNICATION INFORMATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 08-JUL-1994
APPLICATION NUMBER: US 07/
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   1149 amino acids
                                                                                                                                                                                                                                                     904-375-8100
                                                                                                                                                                                                                                           TELEPHONE: 904-272-5800
                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Simi
Matches 752;
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US-08-789-449-2
                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                        QTSVTDYQVNQAANLVECLSDELYPNEKRMIMDAVKEAKRLVQARNILQDTGFNRINGEN 753
                                                                                              RARIRYASTTNLRLFVTIS-----GTRIYSINVNKTMNKGDDLFFNTFDLATIGTA-F 633
                                                                                                                                                                                        989
                                                                                                                                                                                                                                                                                                      GWTGSTGIEVVEGDVLFKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFI 806
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IDSGEELTYEN---YQSYSHRVSYITSPEIKSTGGTV--LGVVPIFGWTHSSASRNNFIY 509
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                                SDKITQI PVVKAHTLVSGTTVI KGPG-FTGGNI LKRTSSGPLAY---TSVSVKSPLSQRY
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/ENTION: No. 5824878el Microorganism and Insecticide
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STREET: 2421 N.W. 41st Street, Suite A-1
STATE: Galnesville
STATE: FL
COUNTRY: US
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Sato, Relichi
Suzuki, No. 5824678ukazu
Ogiwara, Katsutoshi
Sakanaka, Kazunobu
Hori, Hidetaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08789449
Patent No. 5824878
GENERAL INFORMATION:
APPLICANT: Obba, Michio
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.2%; Score 3152; DB 1; Length 1: Best Local Similarity 54.0%; Pred. No. 1.4e-222; Matches 653; Conservative 179; Mismatches 294; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: LambdaGEM-11 library of L. Foncerrada
CLONE: 50C(b)
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA73.C2
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 amino acids
                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: 50C IMMEDIATE SOURCE:
                                                                                                                                                                                                      TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLEGULE TYPE: protein
HYPOTHETICAL: YES
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                                                                                                                                                                                                                                                                                    HYPOTHETICAL: )
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                                                                                                          QTSVTDYQVNQAANLVECLSDELYPNEKRMLWDAVKBAKRLVQARNLLQDTGFNRINGEN
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                                634 TPSNYSDSLTVGADSPASGGEVYVDKFELIPVNATFBAEEDLDVAKKAVNGLFTSKRDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Michaels, Tracy Bllis
APPLICANT: Michaels, Tracy Bllis
APPLICANT: Poncertada, Luis
APPLICANT: Narva, Kenneth B.
TITLE OF INVENTION: Process for Controlling Scarab Pests
TITLE OF INVENTION: with Bacillus thuringiensis Isolates
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1107 NICDDDTGVLSTDQTSYITKTVBFTPSTEQVWIDMSETE 1145
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Gainesville STATE: PL
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US/08/014,941
PILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/808,316
FILING DATE: 16-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08315468
Patent No. 5554534
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                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                          42;
                                                                                                                                                                                                                            Length 1157;
                                                                                                                                                                                                                         Query Match 51.7%; Score 3123; DB 2; Length 11: Best Local Similarity 52.3%; Pred. No. 1.9e-220; Matches 619; Conservative 195; Mismatches 327; Indele
REGISTRATION NUMBER: 30,330
REPERENCE/DOCKET NUMBER: 2121-109P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEFAX: 240345
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                          LENGTH: 1157 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-532-547-5
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                                                                                 QPGVTDYBVNQAANLVECLSDDLYPNBKRLLFDAVREAKRLSBARNLLQDPDFQEINGEN 745
                                                                                                                                                                                                               GSSQGLEIYTIRHQTNRIVKAVPDDDLLPDVPPVNNDGRINRCSBQKYVNSRLEVENR--- 862
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                                                                                                                               GWTGSTGIEVAEGDVLFKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGPI 813
                                                                                                                                              GSSQDLEIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALENNGEN 873
                                                                                                                                                                                                                                                            GNMSSDSHAPSFHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVEEGPLSGETLER 933
                                                                                                                                                                                                                                                                              SVNASSNIQRESIGIQITUTNLFILDRIEFIPVDETYBABTDLBAAKKAVNALFTNTXDGL
   TVGADS------PASGGEVYV-DKFBLIPVNATFRABEDLDVAKKAVNGLFTSKKDAL
                                                                 QTSVTDYQVNQAANLVECLSDBLYPNBKRMLWDAVKEAKRLVQARNLLQDTGFNRINGEN
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APPLICANT: JANSENS, STEFAN
APPLICANT: VAN AUDENGOVE, KATRIEN
APPLICANT: VAN ALS, JEROEN
APPLICANT: VAN ARSSEN, ROEL
TITLE OF INVENTION: INSECTICIDAL PROTEINS.
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSE:
STEMENT: P.O. BOX 747
STERET: P.O. BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BPO)
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CITY: Falls Church
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/532,547
FILING DATE: 06-DBC-1996
CLASSIPICATION: 800
ATTORNEY, AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LAMBERT, BART
APPLICANT: JANSENS, STEFAN
APPLICANT: VAN AUDENBOWE, KATRIEN
APPLICANT: PEFEROEN, MARNIX
APPLICANT: VAN RIE, JEROEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08532547
Patent No. 5861543
GENERAL INFORMATION:
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US-08-532-547-5
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                                                                                                                                                                                IPGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI 1064
                                                                                                                                                                                                SHWDAQVSQQLRVMPNCKYVLRVTARKVGGGDGYVTIRDGAHQBTLTFNACDYDVNGFY 1114
                                                                                                                     MARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPE 1004
                              874
                                                                                                                                                   994
                                                            PHIDTGEIDLINENTGIWVVFKIPTTNGYATLGNLELVEEGPLSGETLERAQQQEQQWQDK 944
                                                                                                                                       HHHKVHLVKAVPDNLVSDTYSDGSCSGINRCDEQHQVDMQLDAEHHPMDCCEAAQTHEFS
                                                                            PNWNSQVSQQPTVQPNYRYVLRVTARKBGVGDGYVIIRDGANGTETLTFNICDDDTGVLS
RHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMSSDSHAFS
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08379656B
Patent No. 5885571
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lambert Bart
APPLICANT: Janeens, Stefan
APPLICANT: Van Audenhove, Katrien
APPLICANT: Peferoen, Marnix
APPLICANT: Peferoen, Marnix
TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND
TITLE OF INVENTION: THEIR INSECTICIDAL PROTEINS
                                                                                                                                                                                                                                                                                                     ADQTSYITKTVEFTPSTEQVWIDMSETEGVFNIESVELVLEBE 1167
                                                                                                                                                                                                                                                                                                                     ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,656B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES
STREET: B110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STREET: VIginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/379,656B
PILING DATE: 23-MAR-1995
RIOR APPLICATION DATE: 39-MAR-1995
RIOR APPLICATION DATE: APPLICATION NUMBER: PCT/RP93/01820
PILING DATE: 12-JULY-1993
RIOR APPLICATION DATE: APPLICATION NUMBER: BP 93400949.9
PILING DATE: 09-APR-1993
RIOR APPLICATION NUMBER: BP 92402358.8
PILING DATE: 27-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: SVENBSOD, LEGDARG R.
REGISTRATION NUMBER: BP 92402358.8
REGISTRATION NUMBER: BP 92402358.8
REGISTRATION NUMBER: BP 92402358.8
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TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 -FPV-SSNFMDYWSGHTLRRSYLNDSAVQEDSYGLITTRATINPGVDGTNR----1EST 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLTREVYTOPIVENRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSEIBFYTTRA 359
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                                                                                                                                                                                                                        1 MARNANGNEYEIIDAPHCGCPSDDDVRYPLASDPNAALQNMYKDYLQMTDEDYTDSYINP
                                                                                                                                                                                                                                                                                     61 BTFISS-STVQTGIGIVQQVLGALGVPPAGQIASPYSRIVGQLWPSSTVSVWEMIMKQVB
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                                                                                                                                                                                                                                                                                                                                                                              DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAKIPSPAISGOEVPLLSVYAQAANIHLLLLRDASIPGAEWGFTPGEISTPYDRQVTRTA
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                                                                                                                                                                                                 1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GADLANYYAQVYGVPYASPTL - - LDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTIDBIPP
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                                                                                                                                                     42;
                                                                                                        Length 1157;
                                                                                                                                                     Indels
                                                                                                        tch 51.7%; Score 3123; DB 2;
al Similarity 52.3%; Pred. No. 1.9e-220;
619; Conservative 195; Mismatches 327;
                  TOPOLOGY: linear
MOLECULE TYPE: protein
amino acid
                                                                                                        Query Match
Best Local Similarity
Matches 619; Conserv
                     ; TOPOLOGY:
; MOLECULE TYI
US-08-379-656B-5
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QY 1 MSPNNQNEYEILDASSSTSV9DNSVRYPLANDQTTTLQNANYKDYLRMSEGENPELFGNP	Qy 61 BTPISS-STVQTGIGIVGQVLGALGVPPAGQIASPYSPIVGQLWPSSTVSVWEMIMKQVE	Qy 120 DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVYTQYIALBLDF 	Qy 180 VAKIPSFAISGGEVPILLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQVTRTA	Qy 240 QYSDYCVKMYNTGLDXLKGTNAASMLKYHQFRREMTLLULDLVALPPNYDTRTYPIETTA : ::	Qy 300 QLTREVYTDPIVFNRETSGGFCRRWSLANSDISPSEVESAVIRSPHLFDILSEIEFYTTRA	Qy 360 GLPLANTEYLEYWVGHSIKYRNTNASSALERNYGTITSNKIKYYDLANKDIPQVRSL	Qy 417 GADLANYYAQVYGVPYASFTLLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP	Qy 475 ENBPLSRGYS-HRLSHITSYSPSKN-ASSPARYGNLPVFAWTHRSADVTMTVYSDKITQI :	Qy 533 PVVKAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSGRYRARIRYASTTN	Qy S93 LRLPVTISGTRIYSINVNKTMNKGDDLTFWTPDLATIGTAFTFSNYSDSLTVGA :	Qy 647 DSFASGGEVYVDKFELIPVNATFBAEEDLDVAKKAVNGLPTSKKDALQTSVTDYQVNQAA :::	Qy 707 NLVECLSDELYPNEKRMLMDAVKEAKRLVQARNLLQDTGPNRINGENGWTGSTGIEVA		Qy 825 RHRANQIVQVPONLLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMSSDSHAFS	Qy 885 PHIDTGEIDLNENTGIWVVPKI PTINGYATLGNLELVEEGPLSGETLERAQQDGQWQDK :	Qy 945 MARKAGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPE :	QY 1005 IPGMAYTSFTELTNRLQQAMNLYDLENAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI	O THE MANUAL THE TREE TO SERVICE TO THE TREE TO SERVICE
QY 945 MARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPE 1004 5	Qy 1005 IPGMYTSPTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI 1064	Qy 1065 PNWNSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDDDTGVLS 1124 : ::	Qy 1125 ADQTSYITKTVEFTPSTEQVWIDMSETEGVENIESVELVLBBE 1167 : : : :	RESULT 11 US-08-455-838-5	2 N 2	; APPLICANT: Jansens, Stefan ; APPLICANT: Van Audenhove, Katrien ; APPLICANT: Pefercen, Marnix ; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND		; STREET: 8110 Gatehouse Road, Suite 500 Bast ; CITY: Parls Church ; STATE: Virginia ; COUNTRY: U.S.A.	; ZIP: 22042 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible	; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: Patentin Release #1.0, Version #1.25 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/455,838	; FILING DATE: 31-MAY-1995 ; PRICR APPLICATION DATA: ; APPLICATION UNMBER: PCT/EP93/01820 ; FILING DATE: 12-JULY-1993	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: BP 93400949.9 ; PILING DATE: 09-APR-1993 ; PRIOR APPLICATION DATA:	# T E 2	; REGISTRATION NUMBER: 30,330 ; REFERENCE/DOCKET NUMBER: 2121-106P ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (703) 205-8000	: (7 2483 FOR CHARA	<pre>j LENGTH: 1157 amino acids j TYPE: amino acid j TOPOLLGY: linear j MOLECULE TYPE: protein</pre>	838-5 atch 51.7%; Score 3123; DB 3; Length 1157; cal Similarity 52.3%; Pred. No. 1.99-220; Tabl. 70.	live 195; Mismatches 327; indels

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995 IPGINYRIYTELSDRLQQASYLYTSRNAVQNGDFNSGLDSWNTTMDASVQODGNMHFLVL 1054
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                                                                                                                                                                         360 -PPV-SSNPMDYWSGHTLRRSYLNDSAVQEDSYGLITTTRATINPGVDGTNR----IEST 413
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                                                                                                    417 GADLANYYAQVYGVPYASFTL - LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP
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US-09-471-177-5
US-09-471-177-5
Sequence 5, Application US/09471177
Patent No. 6448226
GENERAL INFORMATION:
APPLICANT: LAMBERT, BART
APPLICANT: JANSENS, STEFAN
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APPLICANT: LAMBERT, STEPAN
APPLICANT: JANSENS, STEPAN
APPLICANT: WAN AUDENHOVE, KATRIEN
APPLICANT: WAN RIE, JEROEN
APPLICANT: WAN ARSSEN, ROEL
TITLE OF INVENTION: NEW BACTLLUS THURINGIENSIS STRAINS AND THBIR
TITLE OF INVENTION: INSECTICIDAL PROTEINS.
NUMBER OF SEQUENCES:
ADDRESSES: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Palls Church
STREET: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSPNNQNEYELLDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELPGNP
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                                                   1167
                                                                                    1157
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,809
FILING DATE: 02-PEB-1998
CLASSIPICATION: 435
                                                                    1125 ADQTSYITKTVEFTPSTEQVWIDMSETEGVFNIESVELVLEER
                                                                                                                                                                Sequence 5, Application US/09019809
Patent No. 6143550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INPORMATION:
NAME: SYENSON, LEGNARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELER: 248345
INPORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
TRNGTH: 1157 amino acids
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                                                                                                                                                                                                       GENERAL INFORMATION:
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1005 IPGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI 1064
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                                                                                                                                                                                                                             825 RHRANQIVKNVPDNILLPDVLPVNSCGGIDRCSBQQYVDANLALENNGENGNMSSDSHAFS 884
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                                                                                                                                                                                                                                                                                                                                                 NLVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRING--BNGWTGSTGIBVA 764
                                                                                                                                                          DSPASGGEVYVDKPELI PVNATPEAEEDLDVAKKA VNGLPTSKKDALQTSVTDYQVNQAA
                                                                                                                                                                                                                                                                                                                                                                                                                      765 EGDVLPKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFIGSSQDLEIKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                         GADLANYYAQVYGVPYASFTL - - LDKNTGSGSVGGFTYSKPHTTWQVCTQNYNTIDBIPP
                                                                     475 ENEPLSRGYS-HRLSHITSYSPSKN-ASSPARYGNLPVPAWTHRSADVTNTVYSDKITQI
                                                                                                                                                                                                             593 IRLFVTISGTRIYSINVNKTMNKGDDLTFNTF---DLATIG---TAFTFSNYSDSLTVGA
                                                                                                                                        PVVKAHTLVSGTTVIKGPGFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 72, Application US/09002285

Patent No. 6369213

GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Micker, Carol
APPLICANT: Marz, Michelle
APPLICANT: Stockhoff, Brian
APPLICANT: Stockhoff, Brian
APPLICANT: Stockhoff, Brian
APPLICANT: Trockhoff, Trins Applicant: Stockhoff, Brian
APPLICANT: Muller-Cohn, Judy
TITHE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Plorida COUNTRY: USA
                       RESULT 14
US-09-002-285-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 VAKIPSFAISGQEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQVTRTA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 QYSDYCVKWYNTGLDKLKGTNRASWLKYHQFRREMTLLVLDLVALFPNYDTRTYPIETTA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLTREVYTDPIVFNRETSGGFCRRWSLNSDISPSEVESAVIRSPHLFDILSBIBFYTTRA 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
APPLICANT: PEFEROEN, MARNIX
APPLICANT: VAN RIE, JEROEN
APPLICANT: VAN ARRSSEN, ROBL
APPLICANT: VAN ARRSSEN, ROBL
TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR
TITLE OF INVENTION: INSECTICIDAL PROTEINS.
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.7%; Score 3123; DB 4; Length 1:
larity 52.3%; Pred. No. 1.9e-220;
Conservative 195; Mismatches 327; Indels
                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
                                                                                                                           Ξ
                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSER: Birch, Stewart, Kolasch & Birch, STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                          FILLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/019,809
FILING DATE: 02-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: SUENSON, LEONARD R.
REGISTRATION NUMBER: 30,330
FILECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 248345
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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619; Conserv
                                                                                                                                                                                            COUNTRY: USA
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Best Local (
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Matches
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1066 NWNSQVSQQPTVQPNYRYVLRVTARKBGVGDGYVIIRDGANQTETLIPNICDDDTGVLSA 1125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      826 HRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMSSDSHAPSF 885
                                                                                                                                                                                                                                                                                                                                                                                          886 HIDTGEIDLNENTGIWVVPKIPTTNGYATLGNLELVEEGPLSGETLERAQQQEQQWQDKM 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRING--ENGWTGSTGIBVAE 765
                                                                                                                                                                                                                                                                                          GDVLFKDRSLRLTSARRIDTETYPTVLYQQIDESLLKPYTRYKLKGFIGSSQDLBIKLIR 825
                                                            593 LRLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGT----APTFSNYSDSLTVGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        946 ARKRGASEKAYYAAKQAIDRLFADYQDQXLNSGVEMSDMLAAQNLVQSIPYVYNDALPEI
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APPLICANT: Wicker, Carol
APPLICANT: Warvey, Kenneth B.
APPLICANT: Warvey, Kenneth B.
APPLICANT: Stockhoff, Brian
APPLICANT: Stockhoff, Brian
APPLICANT: Stockhoff, Brian
APPLICANT: Stockhoff, Brian
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APPLICANT: Stockhoff, Brian
APPLICANT: Stockhoff, Brian
APPLICANT: Stockhoff, Brian
APPLICANT: Stockhoff, Lioyd & Saliwanchik
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COUNTRY: USA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
FILING DATE:
FLING DATE:
FLING PAPELICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 72, Application US/09589477; Patent No. 6570005; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-09-589-477-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 -PPV-SSNFMDYWSGHTLRRSYLMDSAVQEDSYGLITTTRATINPGVDGTNR----IEST 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALBLDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GADLANYYAQVYGVPYASFTL--LDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTIDEIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENEPLSRGYS-HRLSHITSYSFSKN-ASSPARYGNLPVFAWTHRSADVTNTVYSDKITQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSPNNQNEYBILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSRGENPELFGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 51.3%; Score 3100.5; DB 4; Length Best Local Similarity 52.0%; Pred. No. 8.5e-219; Matches 615; Conservative 196; Mismatches 330; Indels
                                                                                              SOFTWARE: Patent In CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,285
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/86,615
FILING DATE: 1-JUL-1997
PRIOR APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, JAY M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
TELECOMMINICATION INFORMATION:
THELECOMMINICATION INFORMATION:
                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (352) 375-8100
TELEFAX: (352) 375-800
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 amino acids
TYPE: amino acid
STRANDEDNESS: single
                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QXSDYCVGWYNTGLDKI.KGTNAASWI.KYHQFRREMTLLVLDLUVALFPNYDTRTYPI.ETTA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 KYTNYCETWYNTGLDRLRGTNIESWLRYHQPRREWTLVVLDVVALPPYYDVRLYPTGSNP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLPLINNTEYLEYWVGHSIKYKWTNASSALERNYGTITSNKIKY---YDLANKDIPQVRSL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVVKAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTN 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       648 SPASGGEVYVDKPELIPVNATFBAEBDLDVAKKAVNGLFTSKKDALQTSVTDYQVNQAAN 707
                                                                                                                                                                                                                                                                                                                                                                                                                                     61 BTPISS-STVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVB 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENEPLSRGYS-HRLSHITSYSFSKN-ASSPARYGNLPVFAWTHRSADVTNTVYSDKITQI 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                593 LRLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGT----AFTFSNYSDSLTVGAD 647
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                                                                                                                                                                                                                                                                                                                                                                                              1 MSPNNONBYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSBGENPELFGNP
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                                                                                                                                                                                                                                                                                                                         Length 1156;
                                                                                                                                                                                                                                                                                                                        ch 51.3%; Score 3100.5; DB 4; Length al Similarity 52.0%; Pred. No. 8.5e-219; 615; Conservative 196; Mismatches 330; Indels
                    CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDER:
FILING DATE: 1-JUL-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
RECISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C1C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SPECIAL (352) 375-8000
TELEFAX: (352) 375-8000
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08/886,615
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              1-JUL-1997
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
APPLICATION NUMBER:
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Best Local Similarity
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Search completed: June 21, 2004, 10:15:19 Job time : 31 sece